

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 3, 2005, 12:34:58 ; Search time 367.375 Seconds
(without alignments)
4093.201 Million cell updates/sec

Title: US-09-493-480-6
Perfect score: 5078
Sequence: 1 MELAALCRWLLALLPPGA.....TFKGTPTAENPEVLGLDVPV 919

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	4900	96.5	3768	2	US-08-625-101-1 Sequence 1, Appli
2	4900	96.5	3768	2	US-08-356-786-1 Sequence 1, Appli
3	4900	96.5	4473	3	US-09-048-804-1 Sequence 1, Appli
4	4900	96.5	4473	3	US-09-056-105-26 Sequence 26, Appli
5	4900	96.5	4473	4	US-09-663-834A-3 Sequence 3, Appli
6	4900	96.5	4473	4	US-09-441-411-5 Sequence 5, Appli
7	4892	96.3	3768	4	US-09-811-115-2 Sequence 2, Appli
8	4892	96.3	4530	1	US-08-229-515A-9 Sequence 9, Appli
9	4892	96.3	4530	1	US-08-645-865-9 Sequence 9, Appli
10	4892	96.3	4530	3	US-09-167-322-4 Sequence 4, Appli
11	4892	96.3	4530	4	US-09-527-487-1 Sequence 1, Appli
12	4892	96.3	4530	4	US-09-877-177A-11 Sequence 11, Appli

13	4892	96.3	9274	4	US-09-811-115-1 Sequence 1, Appli
14	4134	81.4	3955	1	US-08-229-515A-14 Sequence 14, Appli
15	4134	81.4	3955	1	US-08-645-865-14 Sequence 14, Appli
16	3632	71.5	2385	3	US-09-146-823-3 Sequence 3, Appli
17	3632	71.5	2385	3	US-08-579-823A-3 Sequence 3, Appli
18	3632	71.5	2385	3	US-09-344-195-3 Sequence 3, Appli
19	3471	68.4	1872	3	US-08-422-108-2 Sequence 2, Appli
20	3471	68.4	1872	3	US-08-422-734-2 Sequence 2, Appli
21	1645	32.4	3633	4	US-09-715-249-1 Sequence 1, Appli
22	1645	32.4	3633	4	US-08-475-035-3 Sequence 3, Appli
23	1645	32.4	5532	2	US-09-676-610B-17 Sequence 17, Appli
24	1528.5	30.1	5484	3	US-09-632-580A-3 Sequence 3, Appli
25	1528.5	30.1	5501	1	US-08-484-438-1 Sequence 1, Appli
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27	1435	28.3	4905	1	US-07-978-895-3 Sequence 3, Appli
28	1435	28.3	4905	1	US-08-473-119-3 Sequence 3, Appli
29	1435	28.3	4905	2	US-08-475-352-3 Sequence 3, Appli
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31	1435	28.3	4975	3	US-09-630-706-3 Sequence 3, Appli
32	1435	28.3	4975	4	US-09-949-016-2151 Sequence 2151, Ap
33	1412	27.8	5687	4	US-09-919-039-268 Patent No. 5183884
34	1311	25.8	4545	6	5183884-3 Patent No. 5183884
35	1311	25.8	4545	6	5183884-3 Patent No. 5183884
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37	1032	20.3	1958	4	US-09-867-521-1 Sequence 1, Appli
38	942	18.6	1593	3	US-09-676-610B-25 Sequence 25, Appli
39	942	18.6	1868	1	US-08-658-883B-1 Sequence 1, Appli
40	942	18.6	1868	3	US-09-676-610B-26 Sequence 26, Appli
41	493	9.7	322	1	US-08-421-356-1 Sequence 1, Appli
42	493	9.7	322	3	US-09-046-783-1 Sequence 1, Appli
43	381	7.5	4149	2	US-08-737-715-1 Sequence 1, Appli
44	381	7.5	4723	4	US-09-023-655-1137 Sequence 1137, Ap
45	378	7.4	4041	4	US-09-569-611C-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-625-101-1
; Sequence 1, Application US/08625101
; Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3768 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..3765
 US-08-625-101-1

Alignment Scores:

Pred. No.: 0 Length: 3768
 Score: 4900.00 Matches: 919
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 Best Local Similarity: 73.23% Mismatches: 0
 Query Match: 96.49% Indels: 336
 DB: 2 Gaps: 1

US-09-493-480-6 (1-919) x US-08-625-101-1 (1-3768)

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 DB 61 GCGAGACCCCAAGTGTGCACCGGCACAGACATGAGCTGGGCTCCCTGCCAGTCCCGAG 120
 QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 DB 121 ACCCACTGGACATGTCCGCCACCTCTACAGGGCTGCAGGTGGTGGTGGAGAACCTG 180
 QY 61 GluLeuThrTyrrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
 DB 181 GAACCTCACCTAGCTGCCACCAATGCGCCCTGTCTCTCGAGGATATCCAGAGGTG 240
 QY 81 GlnGlyTyrrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
 DB 241 CAGGGCTACGTCTCATCTGCTCACAACCAAGTGGGCGAGTCCCACTGCAGAGGTGGCG 300
 QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrrAlaLeuAlaValLeuAspAsnGly 120
 DB 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCGGTGTAGACAAATGA 360
 QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 DB 361 GACCCGCTGAACAATACCAACCCCTGTGCAGGGGCTCCCGAGGAGCTGGCGAGGTG 420
 QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValValLeuIleGlnArgAsnProGln 160
 DB 421 CAGCTTCGAAGCCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG 480
 QY 161 LeuCysTyrrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
 DB 481 CTCCTGTACAGGACACAGATTTTGTGGAAAGGACATCTCCACAAGAACCAACAGCTGGCT 540
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 QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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 QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
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 QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
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 DB 1561 TGGGCTCCAGGGCCCAACCCAGTGTGTCAACTGCAGCCAGTTCTCTTGGGGCCAGAGTGC 1620
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 QY 581 AlaAspGlnCysValAlaCysAlaHisTyrrLysAspProPheCysValAlaArgCys 600
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2281	Db	CCCAAGCCCAACAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGCTCCCCA	2340
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653	Qy	-----	653
2401	Db	ATGCCCTATGGCTGCCCTCTTAGACCATGTCCGGGAAACCCGGAGCGCTGGGCTCCAG	2460
653	Qy	-----	653
2461	Db	GACCTGCTGAATGGTGTATGCAGATTGCCAAGGGGATGAGTACTTGGAGGATGTGCGG	2520
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653	Qy	-----	653
2581	Db	ATTACAGACTTCGGGCTGGCTCGCTCTGACATTTGACGAGACAGAGTACCATGCAGAT	2640
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2641	Db	GGGGCAAGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTTCTCCCGCGCGGTTCAAC	2700
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2761	Db	AAACCTTACGATGGGATCCAGGCCCGGAGATCCCTGACCTGTGGAAGAGGGGAGCGG	2820
653	Qy	-----	653
2821	Db	CTGCCCGACCCCCATCTGCACCATTGATGTCTATCATGATCATGTGCAAAATTTGGATG	2880
653	Qy	-----	653
2881	Db	ATTGACTCTGAATGTCTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC	2940
654	Qy	-----GlnAsnGluAspLeuGlyProAlaSerProLeu 	664
2941	Db	AGGACCCCCAGCGCTTTTGGTCAATCCAGAATGAGGACTTGGCGCCAGCCAGTCCCTTG	3000

Qy	665	AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	3001	GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCT	3080
Qy	685	GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyValAcGly	704
Db	3061	GAGAGGTATCTGGTACCCTCCAGAGGGCTTTCTTGCTCAGACCTCTGCCCGGGCGCTGGG	3120
Qy	705	GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr	724
Db	3121	GGCATGTCTCCACACAGGACCGCAGCTCATCTACCAAGGATGCGCGTGGGACCTTGACA	3180
Qy	725	LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly	744
Db	3181	CTAGGGCTGGAGCCCTCTGAAGAGGAGGCGCCACGAGTCTCCATCTGGCACCTCTCGAAGGG	3240
Qy	745	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyValAlaLysGlyLeuGlnSer	764
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Qy	765	LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu	784
Db	3301	CTCCCCACACATGACCCCGACCCCTCTACACGGGTACAGTGAGGACCCACACAGTACCCCTG	3360
Qy	785	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal	804
Db	3361	CCCTCTCAGACTCATGTGCTACGTTGGCCCCCTGACCTGCAGCCCCCAGCCTGAATATGTG	3420
Qy	805	AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla	824
Db	3421	AACAGCGCAGATGTTGGCCCCAGCCCCCTTGGCCCCGAGAGGGCCCTCTGCCTGTCTGCC	3480
Qy	825	ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal	844
Db	3481	CGACCTGCTGGTGCCACTCTGTGAAAGGCCCCACAGACTCTCTCCCCAGGAAAGATGGGGTC	3540
Qy	845	ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln	864
Db	3541	GTCAAAGACGCTTTTGTCTTTGGGGGTGCGTGGAGAACCCCGAGTACTTTGACACCCCGAG	3600
Qy	865	GlyGlyValAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu	884
Db	3601	GGAGGAGCTGCCCTCTAGCCCCACCTCTCTCTGCTTTTACGCCCGAGCCCTTCGACACACCTC	3660
Qy	885	TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr	904
Db	3661	TATTACTGGGACGAGGACCCACACAGAGCGGGGGCTCCACCCAGCACCTTTCAAAGGACA	3720
Qy	905	ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal	919
Db	3721	CTTACGCGCAGAGAACCCAGAGTACTGGGTCTGGACGTGCGAGTG	3765

RESULT 2

US-08-356-786-1
; Sequence 1, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:

Db 1561 ||||| TGGGGTCCAGGGCCACCCAGTGTGTCAGTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaAArgHisCys 560
Db 1621 GTGGAGGAATGCCAGTACTGCAGGGGCTCCCNAGGAGTATGTGAATGCAGGCACGTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1681 TTGCGGTGCCACCTGAGTGTGAGCCCAAGTGGCTCAGTGACCTGTTTGGACCGAG 1740
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrIleAspProPheCysValAlaAArgCys 600
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Db 1861 GGGCATGCCAGCCTTGCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG 1920
QY 641 GlyCysProAlaGluGlnArgAlaSerProIleuThrSer----- 653
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Db 1981 ATTCTGCTGTCGTGCTTGGGGTGGTCTTTGGGATCCTCATCAAGCAGCGCAGCAG 2040
QY 653 ----- 653
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QY 653 ----- 653
Db 2101 ACACCTAGCGAGCGATGCCCAACAGCGCGCAGATCGGATCCTGAAAGAGACGGAGCTG 2160
QY 653 ----- 653
Db 2161 AGNAGTGAAGTGTGGATCTGGCGCTTTTGGACAGCTTACAAAGGGCATCTGGATC 2220
QY 653 ----- 653
Db 2221 CCTGATGGGAGAATGTGAAATTCAGTGGCCATCAAAGTGTGAGGGAACACACATCC 2280
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QY 653 ----- 653
Db 2581 ATTACAGACTTGGGGCTGGCTCGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2640
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Db 2641 GGGGGCAAGGTGCCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCCGCGGTTCCACC 2700
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Db 2761 AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGCTGGAAAAGGGGAGCGG 2820
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Db 2881 ATTGACTCTGAATGTCCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
QY 654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGACGCGCTTTGTGTGTCATCCAGAAATGAGGACTTGGGCCCGCAGCTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACGACACCTTTTACCCTCCTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTTACCCCGACGAGGCTTCTTCTGTCCAGACCTGCCCCGGCGCTGGG 3120
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCATGCTCCACCACAGGACCGCAGCTCATCTACCAGGAGTGGCGTGGGACCTGCACA 3180
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCTCCGAAGGG 3240
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGTTGACCTGGGAATGGGGCAGCCAGGGGCTGCAAGC 3300
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCACACATGACCCCGCCTCTACAGCGGTACAGTGAGGACCCACACAGTACCCCTG 3360
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCTCTGAGACTGATGGCTACGTTGCCCTGACCTGCAGCCCCCAGCTGATATGTG 3420
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCCAGCAGATGTTCCGGCCCCCAGCCCCCTTCGCCCGAGAGGGCCCTCTGCTGCTGCC 3480
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGGTGCCACTCTGGAAGGCCCAAGACTCTCTCCCGAGGAAAGATGGGGTC 3540
QY 845 ValIysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGAGCGTTTTTGCCTTTGGGGTGGCGTGAGAACCCCGAGTACTTTGACACCCCG 3600
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCCCTCAGCCCCCACCCTCTCTCTGCTTCAGCCCGACGCTTCGACACCTC 3660
QY 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACCCAGACCCACCCAGAGCGGGGGCTCCACCCAGCACCTTTCAAAGGACA 3720
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAACCCAGAGTACCTGGGGTCTGGACGTGCCAGTG 3765

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RESULT 3
US-09-048-804-1
; Sequence 1, Application US/09048804
; Patent No. 5968748
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
; TITLE OF INVENTION: HUMAN HER-2 EXPRESSION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,804
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4473 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; ANTI-SENSE: No
; US-09-048-804-1

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservatives: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 2 Gaps: 1

US-09-493-480-6 (1-919) x US-09-048-804-1 (1-4473)

QY 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProProGlyAla 20
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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLeuLeuArgLeuProAlaSerProGlu 40
DB 235 GCGAGCACCAAGTGTGCACCGGCAAGACATGAGCTCGGGCTCCTCGCCAGTCCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 295 ACCACCTGGACATGCTCCGCCACCTCTACAGGGCTGCGAGGTGGTGGAGGAAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 355 GAACCTCACCTACCTGCGCCCAATGCGAGCTGTCTCTCGCAGGATATCCAGGAGGTG 414
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 415 CAGGGCTAGCTGCTCATCTCCTCACACCAAGTGAAGGAGGTCCCTGAGGAGGTGCGG 474
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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DB 475 ATTGTGCGGCGCACCCAGCTCTTTGAGGACAACTATGCTCCCTGGCCGTGTGACAAATGA 534
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DB 535 GACCCGCTGAACAATACCAACCCCTGTCAAGGGGCTCCCCAGGAGGCTGGGGAGCTG 594
QY 141 GlnLeuArgSerLeuThrGluIleLeuGlyGlyValLeuLeuIleGlnArgAsnProGln 160
DB 595 CAGCTTCGAAGCCTCACAGAGATCTTGAAGAGGGGTCTTGATCAGCGGAACCCCCAG 654
QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
DB 655 CTCCTGCTACAGGACACGATTTTGTGAAGAGACATCTTCCACAAGAACCAACAGCTG 714
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 775 GGCTCCCGCTGCTGGGGAGAGATTCTGAGGATTGTCAAGGCTGACGGCCTGCTGTCTGT 834
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
DB 835 GCCGCTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCCACTGCTGCTGCATGAGCAGTGT 894
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 895 GCTGCGGCTGCACGCGGCCCCAAGCACTCTGACTGCTGCCCTGGCTGCCTCAACCCAC 954
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 955 AGTGCATCTGTGAGCTGCACCTGCCCGCTGGTGCCTACCTACACACAGACAGCTTTGAG 1014
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
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QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1255 ATCCAGGAGTTTGTGCGCTGCAAGAAGATCTTTGGAGGCTGGCATTTCTGCCGAGAGC 1314
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1315 TTTGATGGGAGCCAGCCCTCCAACTGCCCCGCTCCAGCCAGCAGAGCTCCCAAGTGT 1374
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaThrProAspSerLeuPro 420
DB 1375 GAGACTCTGGAAGAGATCACAGGTTTACCTATACATCTCAGCATGTGCGGACAGCTGCCT 1434
QY 421 AspLeuSerValPheGlnAsnLeuValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1435 GACCTTCAGCGCTTCCAGAACCTGCAAGTAATCCCGGAGACGAATTTCTGCACAAATGG 1494
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1495 TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGAA 1554
QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
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Db 1555 CTGGCAGTGGAGCTGCTATCCACCATAACACCACCTCTGCTTCGTGCAACGGTG 1614
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1675 GAGGACGAGTGTGGGCGAGGGCTGGCTGCGCCAGCTGTGCGCCGAGGGCACTGC 1734
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1735 TGGGGTCCAGGGCCACCCAGTGTGTCACTGACGACAGTTCCTTGGGGCCAGAGTGC 1794
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1795 GTGGAGGATGCCGAGTACTGCGAGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1854
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Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
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Db 2035 GGGCGCATGCCAGCTTGTGCCCATCAACTGCACCACTCTCTGTGTGGACCTGGATGACAAG 2094
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 2095 GGCTGCCCCCGGACGAGAGCAGCCCTCTGACGTCCTCATCTCTGCGGTGGTGGC 2154
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Qy 653 ----- 653
Db 2875 CACCAGAGTATGTGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934
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Qy 653 ----- 653
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Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
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Qy 665 AspSerThrPheTyrArgSerLeuLeuAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGACCTTTTACCGCTCCTGCTGGAGGACGATGACATGSGGGACCTGGTGGATGCT 3234
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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Db 3355 CTAGGCTGGAGCCCTCTGAGAGGAGGCCCCCAGGTCTTCCACTGGCACCTTCGAAGGG 3414
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
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Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
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Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACACGACAGATGTTCCGGCCCCCAGCCCCCTTGGCCCCGAGAGGGGCTCTGCTGCTGCC 3654
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGCTGGTGCCACTCTGGAAGGGCCCAAGACTCTCTCCCGACGGGAGAAATGGGGTC 3714
Qy 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAGAGCTTTTTCCTTTGGGGTGGCGGTGGAGNACCCCGAGTACTTTGACACCCAG 3774

QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
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RESULT 5

US-09-663-834A-3
; Sequence 3, Application US/09663834A
; Patent No. 6613567
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
; FILE REFERENCE: RTS-0033
; CURRENT APPLICATION NUMBER: US/09/663,834A
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)... (3942)
US-09-663-834A-3

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-663-834A-3 (1-4473)

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Db 235 GCGAGCACCAAGTGTGACCGGCACAGACATGAAGCTCGCGCTCCCTGCCAGTCCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCACCTGGACATGCTCCGCCACCTCTACACAGGGCTGCAGGTGGTCAGAGGAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
Db 355 GAACTCACCTACTGCCCCACCAATGCCAGCTGTCTCTCTGCAGGATATCCAGGAGGTG 414
QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTACGTGCTCATCGCTCACACCAAGTGAAGCAGGTCCCACTGCAGAGGCTGGCG 474
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QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
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QY 141 GlnLeuArgSerLeuThrGlnIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 595 CAGCTTCGAAGCTCACAGAGATCTTGAAGAGAGGGGTCTTATCCAGCGGAACCCCCAG 654
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
Db 655 CTCCTGCTACAGGACACGATTTTGTGAAGAGGACATCTTCCACAGNACCAACAGCTGGCT 714
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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Db 715 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAG 774
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Db 775 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGGATTGTCAAGGCTTGACGGCACTGTCTGT 834
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 835 GCCGGTGGCTGTGCCCGCTGCNAGGGGCACCTGCCACCTGACTGTGCTCATGAGCAGTGT 894
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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Db 1255 ATCCAGGAGTTTGTCTGGCTGCAAGAAGATCTTTGGGAGCTGGCATTTCTGCCGGAGAG 1314
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1315 TTTGATGGGACCCAGCTTCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1374
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
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QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
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DB 2035 GGGCGCATGCCAGCCTTGGCCCATCACTGCACCCACTCTCTGTGTGGACCTGGATGATCAAG 2094
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DB 2515 TATGCTCCCGCCTTCTGGGCATCTGCCTGCACATCCACGCTGCAGCTGGTGACACAGCTT 2574
QY 653 ----- 653
DB 2575 ATGCCCTATGGCTGCCCTTTAGACCATGTCCGGGAAACCGCGGACGCTGGGCTCCAG 2634
QY 653 ----- 653
DB 2635 GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGATGAGTACTCTGGAGGATGTGCGG 2694
QY 653 ----- 653
DB 2695 CTCGTACACAGGACTTGGCCGCTCGGACGTGCTGCTCAAGAGTCCCAACCATGTCAAA 2754
QY 653 ----- 653
DB 2755 ATTACAGACTTCCGGCTGGCTCGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT 2814
QY 653 ----- 653
DB 2815 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGCGGTTTACC 2874
QY 653 ----- 653
DB 2875 CACCAGATGATGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934

QY 653 ----- 653
DB 2935 AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGCTGGAAAAAGGGACCGG 2994
QY 653 ----- 653
DB 2995 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAATGTTGGATG 3054
QY 653 ----- 653
DB 3055 ATTGACTCTGAATGTCCGCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 3114
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
DB 3115 AGSGACCCCGACGCGCTTTGTGTCTATCCAGAATGAGGACTTGGGCCCGACGACCTCCCTG 3174
QY 665 AspSerThrPheTyrArgSerLeuLeuAspAspMetGlyAspLeuValAspAla 684
DB 3175 GACAGCACCTTTTACCGCTCCTGCTGGAGGACGATGACATGGGGACCTTGTGGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3235 GAGGAGTATCTGGTATCCCGCAGCAGGCTTCTTCTGTCCAGACCTTGCCTCCGCGCTGGG 3294
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
DB 3295 GGCATGCTCCACACACGACCGCAGCTCATCTACGAGGAGTGGCGTGGGACCTTGACA 3354
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
DB 3355 CTAGGCTTGAGCCCTCTGAGAGGAGGCCCGCAGGTCTCCACTGGCACCTTCGAAGGG 3414
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
DB 3415 GCTGGCTCCGATGTATTTGATGTGACCTGGGAATGGGGGACAGGGGCTGCAAGC 3474
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
DB 3535 CCTCTGAGACTGATGGCTACGTTGCCCTCCCTGACTGACGCCCGCCAGCTGTATATGTG 3594
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
DB 3595 AACCCGACAGATGTTCCGGCCCCCAGCCCCCTTCCGCCCGAGAGGGGCTCTGCTGCTGCC 3654
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
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QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
DB 3715 GTCAAAGAGTTTTTTCCTTTGGGGTGGCTGGGAGAACCCCGAGTACTTTGACACCCAG 3774
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
DB 3775 GGAGGAGCTGCCCTCAGCCCCCAGCCCTCTCTGCTGCTTCCAGCCAGCTTTCGACCACTC 3834
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
DB 3835 TATTACTGGGACCGAGGCCACCGAGAGCGGGGGCTCCACCCAGCACCTTTCAAAGGACA 3894
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
DB 3895 CCTACGGCAGAAACCCAGAGTACTTGGGTCTGGACGTGCCAGTG 3939

RESULT 6

US-09-441-411-5

; Sequence 5, Application US/09441411

; Patent No. 6734172

; GENERAL INFORMATION:


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; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5

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Alignment Scores:			
Pred. No.:	0	Length:	4473
Score:	4900.00	Matches:	919
Percent Similarity:	73.23%	Conservative:	0
Best Local Similarity:	73.23%	Mismatches:	0
Query Match:	96.49%	Indels:	336
DB:	4	Gaps:	1

US-09-493-480-6 (1-919) X US-09-441-411-5 (1-4473)

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Qy	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
Db	235	GGGAGCACCAAGTGTGACCGGCACACATGAAGCTGGGCTCCTGCCAGTCCGAG	294
Qy	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
Db	295	ACCCACCTGGACATGCTCGGCACCTCTACACAGGGCTGCCAGGTGGTGCAGGGAACCTG	354
Qy	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
Db	355	GAACCTACCTACTCCGCCACCAATGCCAGCTGTCTTCTGCAGGATATCCAGGAGGTG	414
Qy	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	415	CAGGGCTACGTCTCATCGTCCACAACCAAGTAGGCAGAGTCCCACCTGCAGAGGCTGCGG	474
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
Db	475	ATTGTGCGAGGACCACGACTTTTGAGACAACATATGCCCTGGCCGTGTAGACAAATGA	534
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	535	GACCCGCTGAACAATAACACCCCTGTACAGGGGCTCCCACGAGGCGCTTCGGGAGCTG	594
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
Db	595	CAGCTTCGAAGCCTCACAGAGATCTTGAAAGGAGGGGTCTTGATCCACGCGAACC	654
Qy	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
Db	655	CTCTGCTACCGAGACACGATTTTGTGGNAGAGACATCTTCACAGAACACACGAGTGGCT	714
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	715	CTCACACTGATAGACCAACACCGCTCTCGGCGCTGCCACCCCTGTCTCCGATGTGTAAG	774
Qy	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	775	GGCTCCCGTGTGGGGAGAGATTCTGAGATTGTTCAGAGCCCTGAGCCGCACTGTCTGT	834
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisLysGluGlnCys	240
Db	835	GCCGTTGGCTGTGCCGCTGCAAGGGGCACTGCCCACTGACTGCTCCACGAGCAGTGT	894

601 ProSerGlyVallylsProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
1975 CCAGCGGTGAAACCTGACCTCTCTACATGCCATCTGGAGTTTCCAGATGAGGAG 2034
621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
2035 GGGCATGCCAGCTTGGCCCATCACTGACCACTCTCTGTGTGACCTGGATGACAG 2094
641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
2095 GGCTGCCCGCCGAGCAGAGAGCCGCTCTGACGTCCTCATCTCTGCGGTGGTGGC 2154
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2155 ATTCTGCTGCTGTGCTTGGGGTGGTCTTTGGGATCTCTATCAAGCAGCGCAGAG 2214
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2875 CACCAGATGATGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934
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653 ----- 653
2995 CTGCCCCAGCCCCCTCTGCACCATTTGATGTCTACATGATCATGGTCAATGTGGATG 3054
653 ----- 653

3055 ATTGACTCTGAATGTGCGCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 3114
654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
3115 AGGGACCCCGAGCGCTTTGGTGCATCCAGNATGAGACTTGGGCCCGCAGCTCCCTTG 3174
665 AppSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
3175 GACAGCACCTTCTACCGCTCACTGTGTGGAGGACATGATGATGGGGACCTGGTGGATGCT 3234
685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
3235 GAGGAGTATCTGTGTACCCAGCAGGGCTTCTTCTGTCAGACCTGCCCGCGCGCTGGG 3294
705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
3295 GGATGGTCCACACAGCAGCCAGCTCATCTACAGGAGTGGCGTGGGACCTTGACA 3354
725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
3355 CTAGGCTGGAGCGCTCTGAAGAGGAGGCCCGCAGGTCTCCACTGGCACCTCCGAGGG 3414
745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyLeuGlnSer 764
3415 GCTGGCTCCGATGTATTTGATGGTACCTGGGAATGGGGAGTGGCGTGGGACCTGCAAGC 3474
765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
3475 CTCCCGACATGACCCCGCCTCTACAGCGGTACAGTGAGGACCCACAGTACCCCTG 3534
785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
3535 CCTCTGAGACTGATGGCTACGTGGTCCCTGACCTGCAGCCCCCAGCTGTAATATGTG 3594
805 AsnGlnProAspValArgProGlnProSerProArgGluGlyProLeuProAlaAla 824
3595 AACCGCCAGATGTTCGGCCCCAGCCCCCTTCCCGCCGAGAGGGCCCTCTGCTGTCTGCC 3654
825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
3655 CGACCTGCTGTGCCACTCTGGAAAGCCCGCCAGACTCTCTCCCGAGGAAGATGGGGTC 3714
845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
3715 GTCAAGAGCTTTTTCCTTTGGGGTGGCGTGGAGAACCCCGAGTACTTGCACACCCAG 3774
865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
3775 GAGGAGCTGCCCTCAGCCCCCAGCTCTCTCTCTGCTTACGCCAGCTTTCGACCACTC 3834
885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
3835 TATTACTGGAGCAGGACCCAGAGCGGGGGCTCCACCCAGACCTTCAAGGAGCA 3894
905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
3895 CCTACGCGCAGAGAACCCAGAGTACTTGGTGTGGAGCTGCGCAGTGC 3939

RESULT 7

US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16

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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4992.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-811-115-2 (1-3768)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 61 GCGAGCACCAAGTGTGCACCGGCAAGACATGAAGCTCGGCTCCCTGCCAGTCCCGAG 120

QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrgingGlyCysGlnValValGlnGlyAsnLeu 60
DB 121 ACCACCTGGACATGTCCGCGCACCTCTACCAAGGGCTGCCAGGTGGTGAGGGAACCTG 180

QY 61 GluLeuThrTyrrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
DB 181 GAACCTACCTACTGCCACCAATGCCAGCTGTCTCTCTCGAGGATATCAGAGGGTG 240

QY 81 GlnGlyTyrrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 241 CAGGGCTAGCTGTCTATCGCTCACACCAAGTGAGGAGGTCCCACTCGAGAGGTGCGG 300

QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrrAlaLeuAlaValLeuAspGlnGly 120
DB 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAATATGCGCTGGCGGTGTACACAAATGGA 360

QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 361 GACCCGCTGAACATACCAACCCCTGTGCACAGGGGCTCCCGAGGAGGCTGCGGAGCTG 420

QY 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 421 CAGCTTCGAAGCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG 480

QY 161 LeuCysTyrrGlnAspThrIleLeuTrpLysAspIlePheHisLeuAsnGlnLeuAla 180
DB 481 CTCGTGTACAGACACGATTTGTGGAAGGACATCTTCCAAAGAACCAACAGCTGGCT 540

QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAAG 600

QY 201 GlySerArgCysTrpGlyGluSerGluAspCysGlnSerLeuThrArgThrValCys 220
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QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
DB 661 GCGGTGGCTGTGCCCGCTGCAAGGGGCCACTTGCCCACTGACTGTGCTGAGCAGTGT 720

QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 721 GCTGCCGCTGTCAGCGGCCCAAGCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTG 780

QY 261 SerGlyIleCysGlnLeuHisCysProAlaLeuValThrTyrrAsnThrAspThrPheGlu 280
DB 781 AGTGGCATCTGTGAGTGTGACTGCCAGGCCCTGGTCAACCTACACACACAGACACGTTT 840
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QY 301 TyrAsnTyrrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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QY 341 ValCysTyrrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
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QY 401 GluThrLeuGluGluIleThrGlyTyrrLeuTyrrIleSerAlaTrpProAspSerLeuPro 420
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DB 1321 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCACTAGGGAA 1380

QY 461 LeuGlySerGlyLeuAlaLeuIleHisLeuAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGAGTGGAGTGGCCCTCATCCACCATACACCCACCTCTGCTTGTGTGACACGGTG 1440

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QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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DB 2521 CTCGTAACAGGACTTTGGCGCTCGGAACGTGCTCGAAGTGTGTCAGAGTCCCAACCATGTCAA 2580
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DB 3121 GGCATGGTCCACACAGGACCGCAGCTCATCTACCAGGAGTGGCGTGGGACCTTGACA 3180
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DB 3361 CCCTCTGAGACTGATGGCTACGTGGCCCTGACCTGCAGCCCCCAGCCTGAATATGTG 3420
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DB 3421 AACCGACAGATGTTGGGCCCCAGCCCTTGGCCCCGAGAGGGCCCTCTGCTGCTGCC 3480
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
DB 3481 CGACCTGCTGGTGCACCTCTGGAAGGGGCCAAGACTCTCTCCCGAGGAAGATGGGGTC 3540
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
DB 3541 GTCAAAGACGTTTTTGGCTTTGGGGTGGCGTGGAGAACCCGAGTACTTGACACCCAG 3600
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
DB 3601 GGAGGAGCTGCCCTCAGCCCCACCTCTCTGCTTCCAGCCAGCCCTTCGACCAACCTC 3660
QY 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
DB 3661 TATTACTGGGACGAGACCACAGAGCGGGGCTCCACCCAGCACCCTTCAAAGGACA 3720
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
DB 3721 CCTACGGCAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3765

RESULT 8

US-08-229-515A-9
; Sequence 9, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/229,515A
/ FILING DATE: 19 APR 1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PERRYMAN, DAVID G
/ REGISTRATION NUMBER: 33,438
/ REFERENCE/DOCKET NUMBER: 1414.608
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 404-688-0770
/ TELEFAX: 404-688-9880
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4530 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-229-515A-9

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 1 Gaps: 1

US-09-493-480-6 (1-919) x US-08-229-515A-9 (1-4530)
QY 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuProGlyAla 20
DB 151 ATGGAGCTGGCGCTTGTGCGCTGGGGCTCTCTCTCGCCCTCTTGGCCCCCGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 211 GCGAGCACCAAGTGTGCACCGCGCACAGACATGAAGCTCGGCTCTCCCTGCCAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 271 ACCACCTGGAGATGTCTCGCCACCTCTACCAAGGCTGCGAGTGTGTGAGGGAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 331 GAACTCACCTACTGCTCCCAACCAATGCCAGCTGTCTCTCTCCAGGATATCCAGAGGTG 390
QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 391 CAGGGCTACGTGCTCATCGCTCACACCAAGTGAGCGAGGTCCCACTGCAGAGGTGCGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
DB 451 ATTGTGCGAGGACCCAGCTCTTTGAGGACATATGCCCCTGGCCCTGTGACACATGGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 511 GACCCGCTGAACAATACCACTGTGTACAGGGGCTCTCCAGAGGCTGCGGGAGCTG 570
QY 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 571 CAGCTTCGAAGCTTCACAGAGATCTTTGAAGGAGGGGTCTTATCCAGCGGAACCCCCAG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
DB 631 CTCCTGTACAGGACACGATTTTGTGGAAGGACATCTTCCACAGAACCAACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCGACCCCTGTCTCCGATGTGTAAG 750
QY 201 GlySerArgCysTrpGlyLeuSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 751 GGCTCCCGCTGCTGGGGAGAGATTTCTGAGGATTTGTACAGAGCTTCAGCGCTCCTGTGT 810

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QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
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QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 871 GCTGCCGCTGCACGGGCCCCAAGCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 931 AGTGGCATCTGTGAGCTGCACCTGCCCGCCCTGGTGCCTTACCAACACAGACAGCTTTGAG 990
QY 281 SerMetProAsnProGluGlyValArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 991 TCCATGCCAATCCCGAGGGCGGTATACATTCGGCGCCAGCTGTGTGACTGCTGCTGCTGCTGCT 1050
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 1051 TACAACCTACCTTTCTACGGAGCGTGGATCTTGCACCCCTGCTGCTGCCCTGCACAACCAA 1110
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
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QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1171 GTGTGCTATGCTGCGGCATCGAGGACCTTGCAGAGAGGTGAGGGCAGTTACCAAGTGCCTAT 1230
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1231 ATCCAGGAGTTTGTCTGGCTGCAAGAAGATCTTTGGAGCTTCTGCGGAGCTTCTGCGGAGAGC 1290
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
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QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
DB 1351 GAGACTCTGGAAGAGATCACAGTTACTTATACATCTCAGCATGCGCGGACAGCTGCTGCT 1410
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1411 GACCTCAGCGCTTCTCCAGAACCTGCAGTAATCCGGGACGCAATTCGTGCACAAATGGCGCC 1470
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1471 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTGCTGCTGCTGCTGCTGCT 1530
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1531 CTGGGCACTGGAGCTGGCCCTCATCCACCATTAACCCCACTCTGCTTCTGTCACACGGTG 1590
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1591 CCCTGGGACCACTCTTTCGGAAACCCGCAACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1650
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1651 GAGGACGAGTGTGTGGGCGAGGGCTGGCCCTGCCACAGCTGTGCGCCCGAGGGCACTGC 1710
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1711 TGGGGTCCAGGGCCCACTGCTGCTCAACTGCAGCCAGTTCCTTTCGGGGCCAGGAGTGC 1770
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1771 GTGAGGAAATGCCGAGTACTGCAGGGGCTGCCAGGAGTATGTGAATGCCAGGCACTGT 1830
QY 561 LeuProCysHisLeuProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1831 TTCCGCTGCCACCTTGAGTGTGAGGCTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1890
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600

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1891 GCTGACAGGTGTGGCGCTGTGCCCACTATAAGACCTCTCCCTTCTGCGTGGCCGCTGC 1950
601 ProSerGlyVallysProAspLeuSerTyrMetProIleTyrPlysPheProAspGluGlu 620
1951 CCCAGCGGTGAAACCTGACCTCTCTATACGCCCATCTGGAAGTTTCCAGATGAGGAG 2010
621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
2011 GGGCGCATGCCAGCGCTTGCCCCATCACTGCACCCACTCTCTGTGTGGACCTGGATGACAA 2070
641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
2071 GGCTGCCCGCCGAGCAGAGCGAGCCCTCTGACGTCCATCGTCTCTCGCGGTGGTGGC 2130
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2131 ATTCTGCTGTCGTGTCCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGCCAGCAG 2190
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2251 ACACCTAGCGAGCGATGCCCAACAGCGCAGATCGGATCCTGAAAGACGCGAGCTG 2310
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2371 CCTGATGGGGAAGTGTGAAAATTCCAGTGGCCATCAAAGTGTGAGGGAAAAACACATCC 2430
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654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
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3151 GACAGCACCTTTACCGCTCACTGCTGGAGGAGATGACATGGGGACCTTGGTGGATGCT 3210
685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
3211 GAGGAGTATCTGTTACCCAGCAGGCGCTTCTTCTGTCCAGACCTTGCCCGGCGCTGGG 3270
705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
3271 GGCAATGGTCCACACAGGACCGCAGCTCATCTACAGGAGTGGCGTGGGGACCTTGACA 3330
725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
3331 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCTCCGAAGGG 3390
745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
3391 GCTGGCTCCGATGATTTGATGGTGACCTGGGAATGGGGCAGCCCAAGGGGCTGCAAGC 3450
765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
3451 CTCCCAACATGACGCCCGCCTCTACAGCGGTACAGTGGAGACCCACAGTACCCCTG 3510
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3511 CCTCTGAGACGTATGGCTAGCTTGGCCCCCTGACCTGCAGCCCCCAGCCTGAATATGTG 3570
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3751 GGAGGAGCTGCCCTCAGCCCCCAGCCCCCTCTCTGCTGCTTCCAGCCCGAGCTTCGACACCTC 3810
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3811 TATTACTGGGACCCAGACCCACAGAGCGGGGGCTCCACCCAGCACCTTTCAAAGGACA 3870
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RESULT 9

US-08-645-865-9
; Sequence 9, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUIDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:

/ ADDRESSES: NEEDLE & ROSENBERG PC
 / STREET: 127 Peachtree Street, Suite 1200
 / CITY: Atlanta
 / STATE: Georgia
 / COUNTRY: usa
 / ZIP: 30303
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/645,865
 / FILING DATE: 14 MAY 1996
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: PERRYMAN, DAVID G
 / REGISTRATION NUMBER: 33,438
 / REFERENCE/DOCKET NUMBER: 1414.608
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 404-688-0770
 / TELEFAX: 404-688-9880
 / INFORMATION FOR SEQ ID NO: 9:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 4530 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / US-08-645-865-9

Alignment Scores:

Pred. No.: 0 Length: 4530
 Score: 4892.00 Matches: 918
 Percent Similarity: 73.15% Conservative: 0
 Best Local Similarity: 73.15% Mismatches: 1
 Query Match: 96.34% Indels: 336
 DB: 1 Gaps: 1

US-09-493-480-6 (1-919) x US-08-645-865-9 (1-4530)

QY 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProGlyAla 20
 DB 151 ATGGAGCTGGCGGCTTGTGGCGCTGGGGCTCTCTCGCCCTCTTGGCCCGCGAGCC 210
 QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 DB 211 GCGAGACCAAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCCTGCCAGTATCCCGAG 270
 QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 DB 271 ACCACCTGGACATGCTCCGCCACCTCTACCAAGGCTGCCAGTGGTGCAGGGNAACCTG 330
 QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
 DB 331 GAACCTCACCTACTGCCACCAATGCAGCCGTGCTCTCTCCAGGATATCCAGGAGGTG 390
 QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
 DB 391 CAGGGCTACGTGCTCATCGCTCACACCAAGTGAGCGAGTCCCACTGCAGAGGCTGGCG 450
 QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
 DB 451 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGCCCTGCCAGTATGGA 510
 QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 DB 511 GACCGGCTGAACAATACCACTCTTTGAGGACAACTATGCCCTGCCCTGCCAGGCTGG 570
 QY 141 GlnLeuArgSerLeuThrGlnIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
 DB 571 CAGCTTCGAGAGCTCACAGAGATCTTGAAGAGGGGTCTTGATCAGCGGAACCCCGAG 630
 QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180

DB 631 CTCTGCTACCAAGCACCATTTTGTGGAAGGACATCTTCCACAAGACAACACAGCTGGCT 690
 QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
 DB 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAAG 750
 QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
 DB 751 GGCTCCCGCTGCTGGGAGAGATTCTGAGGATTGTCAAGGCTGACGGCACTGTCTGT 810
 QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
 DB 811 GCGGTGGCTGTGCCCGCTGCAGGGGCCACTTGCCTGCCCTGCCCTGCCCTGCCCTGCC 870
 QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 DB 871 GCTGCCGCTGCACGGGCCCAAGCACTGTACTGCCCTGGCTGCCCTGCCCTGCCCTGCC 930
 QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
 DB 931 AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTACACACAGACACGTTTGA 990
 QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
 DB 991 TCCATGCCCAATCCCGAGGGCGGTATACATTTGGGGCCAGCTGTGTGACTGCCCTGCC 1050
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 DB 1051 TACAACCTACCTTTCTACGGAGCTGGGATCCTGCACCCCTCGTCTGCCCTGCCCAACCA 1110
 QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
 DB 1111 GAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAAGATGCGCAGAGCCCTGTGCCGA 1170
 QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
 DB 1171 GTGTGCTATGTCTGGGCATGGAGCATTGGAGAGGTGAGGGCAGTTACCAAGTGCCT 1230
 QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
 DB 1231 ATCCAGGAGTTTGTGCTGGCTGCAAGAAGATCTTTGGGAGCTGGCATTTCTGCCGAGAG 1290
 QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
 DB 1291 TTTGATGGGGACCCAGCCCTCCAACTGCCCGCTCCAGCCAGAGCAGCTCCCAAGTGT 1350
 QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
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 DB 1411 GACCTCAGCGCTTTCAGAACCTTCAAGTAATCCGGGACCGAATTTCTGCACAAATGGCG 1470
 QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
 DB 1471 TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGGCTCACTGAGGGA 1530
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 DB 1531 CTGGCAGTGGACTGGCCCTCATCCACCAACCCACCTCTGCTTCTGTCACACCGGTG 1590
 QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
 DB 1591 CCCTGGGACCAAGCTCTTTCCGAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCA 1650
 QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
 DB 1651 GAGGACGAGTGTGTGGGCGAGGGCTTGGCTGCCACCAAGCTGTGGCCCGAGGGCACTGC 1710
 QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540

Db	1711	TGGGGTCCAGGGCCACCAGTGTGTCAACTGCGAGCCAGTTCCTTCGGGGCCAGGAGTGC	1770
Qy	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaAatHisCys	560
Db	1771	GTGGAGGAATGCCGAGTACTGACGGGCTCCACAGGAGATATGTGAATGCCAGGCACTGT	1830
Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
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Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaAatCys	600
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Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu	620
Db	1951	CCCAGCGGTGTGAACCTGACCTCTCTACATGCCATCTGGAGTTTCCAGATGAGGAG	2010
Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
Db	2011	GGCGCATGCCAGCCTTGCCCATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG	2070
Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer-----	653
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Db	2131	ATTCTGCTGCTGTGGTCTTTGGGGTGGTCTTTGGGATCCTCATCAAGACGCGCAGCAG	2190
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Db	2191	AAGATCCGGAAGTACACGATCCGAGACTGCTGCAGGAACGGAGCTGGTGGAGCCGCTG	2250
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Db	2311	AGGAAGTGAAGTGTGGTCTGGCGCTTTTGGCACAGTCTACAAAGGCATCTGGATC	2370
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Db	2371	CCTGATGGGAGAATGTGAATTTCCAGTGGCCATCAAAGTGTGAGGGAACACATCC	2430
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Qy	653	-----	653
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Db	2971	CTGCCCGAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGGTCAAAATGTTGGATG	3030
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Db	3031	ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCGCATGGCC	3090
Qy	654	-----GlnAsnGluAspLeuGlyProAlaSerProLeu	664
Db	3091	AGGACCCCGCAGCGCTTTTGGTTCATCCAGAAATGAGGACTTGGGCCCGCAGCTCCCTTG	3150
Qy	665	AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	3151	GACAGCACCTTCTACCGCTCCTCTGGAGGACATGACATGGGGACCTTGGTGGATGCT	3210
Qy	685	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	704
Db	3211	GAGGAGTATCTGTGTACCCCGCAGCAGGCTTCTCTGTCCAGACCTGCCCCGGCGCTGGG	3270
Qy	705	GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr	724
Db	3271	GGCATGTCTCCACACAGCAGCAGCTCATCTACCAGGAGTGGCGTGGGACCTGACA	3330
Qy	725	LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly	744
Db	3331	CTAGGCTGGAGCCCTCTGAGAGGAGGCCCCAGGTCTCCACTGGCACCTCTCGAAGGG	3390
Qy	745	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer	764
Db	3391	GCTGGCTCCGATGTAATTTGATGTGACCTGGGAATGGGGGACGCCAAGGGGCTGCAAGC	3450
Qy	765	LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu	784
Db	3451	CTCCCGACACATGACCCCGCCTCTACAGCGGTACAGTGAGGACCCCGACAGTACCCCTG	3510
Qy	785	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal	804
Db	3511	CCCTCTGAGACTGATGGCTACGTTGCCCTCCCTGACCTGCGAGCCCGCCAGCTGATATGTG	3570
Qy	805	AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla	824
Db	3571	AACCGCCAGATGTTCCGGCCCGCAGCCCTTCCGCCCGAGAGGGCCCTCTGCTGCTGCC	3630
Qy	825	ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal	844
Db	3631	CGACCTGCTGGTGCCACTCTGGAAGGGGCCAAGACTCTCTCCCGAGGAGAAATGGGGTC	3690
Qy	845	ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln	864
Db	3691	GTCAAGAGCTTTTTCCTTTGGGGGTGCGTGGAGAACCCCGAGTACTTTGACACCCCG	3750
Qy	865	GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu	884
Db	3751	GGAGGAGCTGCCCTCAGCCCCCAGCCCTCTCTCTGCTTCCAGCCAGCTTTCGACACCTC	3810
Qy	885	TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr	904
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Qy	905	ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal	919
Db	3871	CTTACGGCAGAAACCCAGAGTACTTGGGTCTGGAGCTGCCAGTG	3915

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121	QY	AppProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
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141	QY	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
571	DB	CAGCTTCGAAGCCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG	630
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631	DB	CTCTGCTACGAGACACGATTTTGTGGAGGACATCTTCCACAAGAAACCAACGCTGGCT	690
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691	DB	CTCACACTGATAGACACCAACCGCTCTCGGGCTTGCACCCCTGTCTCCGATGTGTNAG	750
201	QY	GlySerArgCyseTrpGlyGluSerSerGluAspCyseGlnSerLeuThrArgThrValCyse	220
751	DB	GGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATGTGCAGAGCCTGCACGGCACTGTCTGT	810
221	QY	AlaGlyGlyCyseAlaArgCyseLysGlyProLeuProThrAspCyseHisGluGlnCyse	240
811	DB	GCCGGTGGCTGTGCCCGCTGCAGAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT	870
241	QY	AlaAlaGlyCyseThrGlyProLysHisSerAspCyseLeuAlaCyseLeuHisPheAsnHis	260
871	DB	GCTGCCGGCTGCACAGGGCCCCAAGCACTCTGACTGCTTGGCCCTGCCCTTCAACCAAC	930
261	QY	SerGlyIleCyseGluLeuHisCyseProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
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1291	DB	TTTGATGGGGACCCAGCCTCCAACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGTTT	1350
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QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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RESULT 11
US-09-527-487-1
; Sequence 1, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)...(3915)
US-09-527-487-1

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

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Db 391 CAGGGCTACGTGCTCATCGCTCACACCAAGTGAAGCAGGTCCCACTCGAGAGGCTGCGG 450
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QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3211 GAGGATATCTGGTACCCCGCAGCAGGCTTCTTCTGTCCAGACCTGCCCGCGCTGGG 3270
QY 705 GlyMetValHisHisArgHisArgSerSerSerThrArgSerGlyGlyAspLeuThr 724
DB 3271 GGCATGGTCCACACAGGACCGCAGCTCATCTACAGAGAGTGGCGGTGGGAGACCTGACA 3330
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
DB 3331 CTAGGCTGGAGCCCTCTGAGAGGAGGCGCCCGCAGTCTCCACTGCGACCTCCGAAGGG 3390
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
DB 3391 GCTGGCTCCGATGTATTTGATGTGACCTGGGAATGGGGCAGCCCAAGGGGCTGCAAGC 3450
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
DB 3451 CTCCCCACACATGACCCCGCAGCCCTCTACAGCGGTACAGTGAGGACCCACAGTACCCTG 3510
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
DB 3511 CCTCTGAGACTGATGGCTACGTGGCCCCCTGACCTGACGCCCCCGACGCTGATATGTG 3570
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
DB 3571 AACCCAGCAGATGTTCCGGCCCCCAGCCCCCTTCGCCCGAGAGGGCCCTCTGCTGCTGCC 3630
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
DB 3631 CGACCTGCTGGTGCCCATCTCGAAGAGGGCCAAAGACTCTCTCCCGCAGGGAAGATGGGGTC 3690
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
DB 3691 GTCAAGAGCTTTTTCCTTTGGGGTGCCTGGAGAACCCCGAGTACTTGACACCCCGAG 3750
QY 865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 884
DB 3751 GGAGGAGCTGCCCTCAGCCCCCAGCTCTCTCTGCTTCCAGCCCGACGCTTCGACACCTC 3810
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
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Db 3811 TATTACTGGACGACGACCCACAGCGGGGGCTCCACCCAGCACCTTCAAAGGGACA 3870
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3871 CCTACGGCAGAAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3915

RESULT 12
US-09-877-177A-11
; Sequence 11, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-11

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-877-177A-11 (1-4530)
Qy 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 151 ATGGAGCTGGCGCCTTGTGCCGCTGGGGGCTCCTCCTCGCCCTCTTGCCCCCGGAGCC 210
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 211 GCGAGCACCAAGTGTGCAACCGGCACAGACATGAAGCTCGCGCTCCCTGCCAGTCCCGAG 270
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnValAsnLeu 60
Db 271 ACCCACTGGACATGCTCCGCCACCTCTACCAAGGCTGCCAGGTGGTGGAGGAACCTG 330
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
Db 331 GAACTCACCTACCTGCCACCAATGCGAGCCTGTCTCTTCTGCAGGATATCCAGGAGGTG 390
Qy 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGCTACGTGCTCATCGCTCACACCAAGTGAGGCAGGTGCCACTGCAGAGGTGGCG 450
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 451 ATTGTGCGAGGACCCAGCTCTTTGGAGCACTATGCGCCCTGGCCGTGTGACACATGGA 510
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 511 GACCCGCTGAACAATACCAACCCCTGTGCAGGGGCTCCCGAGGAGGCTGGCGGAGCTG 570
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 571 CAGCTTCGAAGCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCCGAG 630
Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLeuAsnGlnLeuAla 180
Db 631 CTCGTCTACGAGACACGATTTTGTGGAAGGACAATCTTCCAAAGAACCAACAGCTGGCT 690
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 691 CTCACTGATAGACACCAACCGCTCTCGGGCTCCACCCCTGTCTCCGATGTGTAAG 750
Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 751 GGTCCCGCTGCTGGGGAGAGATTTCTGAGGATTTCTAGAGCTGACGCGCACTGTCTGT 810
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 811 GCCGTGGCTGTGCCCGCTGCAAGGGGCACTGCCCCACTGACTGCTGCCATGAGCAGTGT 870
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
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Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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Qy 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1231 ATCCAGGAGTTGTCTGGCTGCAAGAAGATCTTTGGAGCTTGGCATTTCTGCCGAGAGC 1290
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Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
Db 1351 GAGACTCTGGAAAGAGATCACAGTTACCTATACATCTCAGCATGGCCGAGCAGCTGCCT 1410
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1411 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGAGCAGAAATCTGCACAAATGGCGC 1470
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1471 TACTCGCTGACCCCTCAAGGGCTGGGCATCAGCTGGCTGGGGCTCGGCTCACTAGAGGAA 1530
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1531 CTGGCAGTGGACTGGCCCTCATCCACCATAAACCCACCTCTGCTTCGTGTCACAGGTG 1590
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1591 CCCTGGGACCAAGCTCTTTCCGNAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCA 1650
Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1651 GAGGACAGTGTGTGGGCGAGGGCTGGCCCTGCCACAGCTGTGGCGCGGAGGCACTGC 1710
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1711 TGGGTCCAGGGCCCAACCCAGTGTGTCAACTGCACCCAGTCTCTTCGGGGCCAGGAGTGC 1770
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
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Db TTGCGGTGCCACCTGAGTGTGACGCCCCAGAAATGGCTCAGTGACCTGTTTGGACCGGAG 1890
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Qy 653 ----- 653
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Qy 654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db AGGGACCCCGCGCTTTGTGGTGCATCCAGAAATGAGACTTGGGCCCGCAGCAGTCCCTTG 3150
Qy AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db GACAGCACCTTCTTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGGTGATGCT 3210
Qy GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db GAGGATATCTGTATACCCAGCAGGGCTTCTTCTGTCCAGACCTTGCCCGGGCGCTGGG 3270
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Qy AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db AACCGCCAGATGTTGGCCCCAGCCCCCTTCCCGCCGAGGGGCCCTCTGCTGCTGCC 3630
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Qy ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
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Qy GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db GGAGGAGCTGCCCTCAGCCCCACCTCTCTGCTGCTTCCAGCCAGGCTTCGACCAACCTC 3810
Qy TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db TATTACTGGGACCCAGGACCCAGAGCGGGGGCTCCACCCAGCACCTTCAAAGGAGCA 3870
Qy ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db CCTACGCGCAGAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3915

RESULT 13

US-09-811-115-1

; Sequence 1, Application US/09811115

; Patent No. 6632979

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/ GENERAL INFORMATION:
/ APPLICANT: Erickson, Sharon
/ APPLICANT: Schwall, Ralph
/ APPLICANT: King, Kathleen
/ TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
/ FILE REFERENCE: GENENT.034A
/ CURRENT APPLICATION NUMBER: US/09/811,115
/ CURRENT FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/189,844
/ PRIOR FILING DATE: 2000-03-16
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 9274
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Vector Sequence
US-09-811-115-1

Alignment Scores:
Pred. No.: 0 Length: 9274
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-6 (1-919) x US-09-811-115-1 (1-9274)
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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 1791 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCCTGCCAGTCCCGAG 1850
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 1851 ACCCACTGGACATGCTCCGCCACCTCTACCAAGGGCTGCGAGTGTGAGGGAACCTG 1910
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
DB 1911 GAACTCACCTACCTGCCACCAATGCCAGCTGCTCTCTCCAGGATATCCAGAGGCTG 1970
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 1971 CAGGGCTACGCTGCTCATCGCTCACAAACCAAGTGAGGAGGCTCCCACTGCAGAGGCTGCGG 2030
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
DB 2031 ATTGTCGAGGACCCAGCTCTTTGAGGACAACTATGCGCTGGCGTGTAGACAAATGGA 2090
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 2091 GACCCGCTGAACAATACCACTGTGCAGGGGCTCCCGAGGAGCTGCGGAGGCTG 2150
QY 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 2151 CAGCTTCGAAGCCTCACAGAGATCTTTGAAAGGAGGGGCTTGTATCCAGCGGAACCCCGAG 2210
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DB 2211 CTCCTGTACAGACACGATTTTGTGGAAGGACATCTTCCAAAGAACCAACCAAGCTGGCT 2270
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
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QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 2331 GGCTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTTGTAGAGCTTGTAGAGCTTGACGGCCTGCTGT 2390
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QY 281 SerMetProAsnProGluGlyValArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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DB 2931 GAGACTCTGGAGAGAGATCACAGTTACTATATACATCTCAGCATGCGCGGACAGCTGCCT 2990
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 2991 GACCTCAGCGCTTCTCAGAACCTCGCAAGTAAATCCGGGAGCAGAAATCTGCACAAATGGCGC 3050
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
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QY 461 LeuGlySerGlyLeuAlaLeuIleHisLeuAsnThrHisLeuCysPheValHisThrVal 480
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QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
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QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 3411 TTGCCGTGCCACCTTGAGTGTGAGCCCGGAGAAATGGCTCAGTGCCTGTGTGTGGACCGGAG 3470
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QY 581 AlaAspGlnCysValAlaCysAlaHisTyrIlyAspProProPheCysValAlaAArgCys 600
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QY 641 GlyCysProAlaGluGlnAArgAlaSerProIleThrSer----- 653
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Db 4431 CACCAGATGATGTGTGAGATTATGTGTGACTGTGTGGAGCTGATGATTTTGGGGCC 4490
QY 653 ----- 653
Db 4491 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTGGAAGGGGAGCGG 4550
QY 653 ----- 653

Db 4551 CTGCCCCAGCCCCCATCTCTGCACCATTTGATGTCTACATGATCATGTCAAATGTGGATG 4610
QY 653 ----- 653
Db 4611 ATTGACTCTGAATGTTCGGCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 4670
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 4671 AGGGACCCCGAGCGCTTTGTGGTCACTCCAGAAATGAGACTTGGGCCCGAGCAGTCCCTTG 4730
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 4731 GACAGACCTTCTACCGCTCACTGTGTGGAGGACGATGACATGGGGACCTCGTGGATGCT 4790
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 4791 GAGGAGTATCTGTGTACCCAGCAGGCTTCTTCTGTCCAGACCTGCCCGCGCGCTGGG 4850
QY 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 4851 GGCATGGTCCACCACAGGCACCGCAGCTCATCTACCAGGAGTGGCGTGGGACCTGCACA 4910
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 4911 CTAGGCGCTGGAGCCCTCTGAAGAGGAGGCCCGCCAGGTCTCCACTGGCACCCTCCGAAGGG 4970
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaIysGlyLeuGlnSer 764
Db 4971 GCTGGCTCGATGTATTGATGTGACTGGGAAATGGGGCAGCCCAAGGGGCTGCAAGC 5030
QY 765 LeuProThrHisAspProSerProLeuGlnAArgTyrSerGluAspProThrValProLeu 784
Db 5031 CTCCCCACACATGACCCCGCCCTCTACAGCGGTACAGTGAGGACCCACACAGTACCCTG 5090
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 5091 CCCTCTGAGACTGATGGCTACGTGTGCCCTGACCTGCAGCCCCCAGGAGGAGGCTCTGCTGCTGCTG 5150
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 5151 AACCAGCCAGATGTTCGGCCCCAGCCCCCTTCGCCCGAGAGGGGCTCTGCTGCTGCTGCC 5210
QY 825 ArgProAlaGlyAlaThrLeuGluAArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 5211 CGACCTGTGTGCCACTCTGGAAAGGGCCAGACTCTCTCCCAGGGAAGAATGGGGTC 5270
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 5271 GTCAAAGACGTTTTTTCCTTGGGGGTGCGGTGGAGAACCCCGAGTACTTTGACACCCCGAG 5330
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 5331 GGAGGAGCTGCCCTCAGCCCCACCTCTCTGCTGCTTACGCCAGGCTTCGACCAACTC 5390
QY 885 TyrTyrTrpAspGlnAspProProGluAArgGlyAlaProProSerThrPheLysGlyThr 904
Db 5391 TATTACTGGGACCCAGACCCACAGAGCGGGGGCTCCACCCAGACCTTCAAAGGAGACA 5450
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 5451 CCTACGCGAGAGAACACAGAGTACCTGGGTCTGGACGTGCCAGTG 5495

RESULT 14

US-08-229-515A-14
; Sequence 14, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUIDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
 ADDRESSEE: NEEDLE & ROSENBERG PC
 STREET: 127 Peachtree Street, Suite 1200
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: usa
 ZIP: 30303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/229,515A
 FILING DATE: 19 APR 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PERRYMAN, DAVID G
 REGISTRATION NUMBER: 33,438
 REFERENCE/DOCKET NUMBER: 1414.608
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-688-0770
 TELEFAX: 404-688-9880
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3955 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-229-515A-14

Alignment Scores:
 Pred. No.: 0 Length: 3955
 Score: 4134.00 Matches: 781
 Percent Similarity: 65.47% Conservative: 42
 Best Local Similarity: 62.13% Mismatches: 96
 Query Match: 81.41% Indels: 338
 DB: 1 Gaps: 3

US-09-493-480-6 (1-919) x US-08-229-515A-14 (1-3955)

1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuAlaLeuLeuProGlyAla 20
 26 ATGGAGCTGGCGCCTGGTGGCGCTGGGGGTCTCTCTCGCCCTCGCCGCCCGGAATC 85
 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 86 GCGGGCACCAAGTGTGTACCGGCACAGACATGAAGTTGCGGCTCCCTGCCAGTCTGTGAG 145
 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 146 ACCACCTGGACATGCTCCGCCACCTGTACCAAGGCTGTACAGTAGTGCAGGGCAACTTG 205
 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
 206 GAGCTTACCTACGTGCTGCCAATGCCAGCTCTCATTCTCGAGGACATCCAGGAAGTT 265
 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
 266 CAGGGTTACATGCTCATCGCTCACACACAGGTGAAGCGCTCCCACTGCAAAAGGTGGCG 325
 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
 326 ATCGTGAGAGGACCCAGCTCTTTGAGGACAGTAGTCCCTGGCTGTGTAGAACCGA 385
 121 AspProLeuAsnAsnThrThrProValThr---GlyAlaSerProGlyGlyLeuArgGlu 139
 386 GATCTTCAGGACAAATGTCGCGCTCCACCCAGGCGAGAACCCAGAGGGGTGCGGGAG 445
 140 LeuGlnLeuArgSerLeuThrGluIleLeuLysGlyValIleGlnArgAsnPro 159
 446 CTGCAGCTTCGAAGTCTCAGAGATCTCGAAGGGGAGGAGTTTGTATCGTGGGAACCTC 505

160 GlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeu 179
 506 CAGCTCTGCTACCAGGACATGGTTTGTGAAGGAGCTTCCGCAAGATTAACCAACTG 565
 180 AlaLeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCys 199
 566 GCTCTGTGATATAGACACCAATGTTCCGGGCTGTCCACCTTGTGCCCCCGCTGC 625
 200 LysGlySerArgCysTrpGlyLysSerGluAspCysGlnSerLeuThrArgThrVal 219
 626 AAAGACAATCACTGTTGGGTGAGAGTCGGGAAGACTGTACAGATCTTGATCGCACCATC 685
 220 CysAlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGln 239
 686 TGTACCACTGGTTGTGCGGGTGAAGGGCCGGCTGCCCACTGCTGCTCCATGAGCAG 745
 240 CysAlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsn 259
 746 TGTGCCGAGGCTGCACGGGCCCAAGCATCTGACTGCTGCTGCTGCCCTCCACTTCAAT 805
 260 HisSerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPhe 279
 806 CATAGTGTATCTGTGAGCTGCACCTGCCAGCCCTCGTCACTACCAACACAGACACTTT 865
 280 GluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCys 299
 866 GAGTCCATGCACACCTGAGGGTGCCTACACTTTGGTGCAGCTGCGTGACCACTGC 925
 300 ProTyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsn 319
 926 CCTTACAACCTACTGCTACGGAAGTGGATCCTGCACCTCTGCTGCTCCCGGAATAC 985
 320 GlnGluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAla 339
 986 CAAGAGGTCAAGCTGAGGAGCGAAACAGAGCTTGTGAGAAATGAGCAAGCCCTGTGCT 1045
 340 ArgValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAla 359
 1046 CGAGTGTCTATGTTCTGGGCATGGAGCACCTTCAGGGGCGAGGGCCATCACCAGTGAC 1105
 360 AsnIleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGlu 379
 1106 AATGTCAGAGGATTTGATGGCTGCAAGAAGATCTTTGGAGAGCTGGCATTTTTCGGGAG 1165
 380 SerPheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnVal 399
 1166 AGCTTTGATGGGAGCCCTCTCCGGCATTTGCTCCGGCATTTGCTGAGAGCTTCAAGTG 1225
 400 PheGluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeu 419
 1226 TTCGAAACCTGGAGGAGATCACAGTTTACCTGTATCATCTCAGCATGGCCAGACAGTCTC 1285
 420 ProAspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGly 439
 1286 CGTGACCTCAGTGTCTTCAGAACCTTCGAATCATTCGGGGACGGATTTCTCCACCATGCG 1345
 440 AlaTyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArg 459
 1346 GGTACTCATTTAGACTGCAAGGCTGGGATTCACATCGCTGGGGCTGGCTGCTGCTGCGG 1405
 460 GluLeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThr 479
 1406 GAGCTGGCAGTGGATTTGGCTCTGATTCCACGCAAGCCCATCTCTGCTTTGTACACACT 1465
 480 ValProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArg 499
 1466 GTACCTTGGGACAGCTCTTCGGGAACCCACATCAGGCGCTGCTCCACAGTGGGAACCGG 1525
 500 ProGluAspGlu---CysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGly 518
 1526 CCGGAAGAGGACTGTGGCTCTCGAGCGGCTGGTGTGTAACCTCACTGTGCTGCCACCGG 1585
 519 HisCysTrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGln 538

Db 1586 CATGCTGGGGGCGAGGGCCACCCAGTGTCACTGCGAGTCATTTCTTCGGGGCCAG 1645
QY |||||
Db 539 GluCysValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArg 558
QY |||||
Db 1646 GAGTGTGGAGGAGTCCGAGTATGGAAGGGGCTCCCCGGGAGTATGTAGTGACAAG 1705
QY |||||
Db 559 HisCysLeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGly 578
QY |||||
Db 1706 CGCTGTGCGGTGTCAACCGAGTGTCAAGCTCAAAACAGCTCAGAGACCTGCTTTGGA 1765
QY |||||
QY ProGluAlaAspGlnCysValAlaCysAlaHisTyrIlyAspProProPheCysValAla 598
Db 1766 TCGGAGGCTGATCAGTGTGCGAGCTGCGCCACTACAAGGACTCGCTCTGTGTGGCT 1825
QY ArgCysProSerGlyValIlyProAspLeuSerTyrMetProIleTyrIlyPheProAsp 618
Db 1826 CGCTGCCCCAGTGGTGAACCGGACCTCTCTACATGCCCATCTGGAAGTACCCGGAT 1885
QY GluGluGlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAsp 638
Db 1886 GAGGAGGGCATATGCCAGCGGTGCCCATCAACTGCACCCACTCTCTGTGTGGATCTGGAT 1945
QY AspIlyGlyCysProAlaGluGlnArgAlaSerProLeuThr----- 652
Db 1946 GAACGAGGCTGCCAGAGAGCAGAGAGCCAGCCCGGTGACATTTCATTGCAACTGTA 2005
QY :|||:|
QY 639 652
Db 2006 GAGGGCGTCTGTGTCTCTGATCTTAGTGGTGGTCTGCGAGAACTGAGTTAGTGGAG 2065
QY 652
Db 2066 AGACAGAAGATCCGGAAGTATACGATCGGTAGGTCTGCGAGAACTGAGTTAGTGGAG 2125
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Db 2126 CGCTGACGCGCCAGCGAGCAATGCCAACAGGCTCAGATCGGATCTTAAAGAGAG 2185
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Db 2186 GAGCTAAGNAGGTGAAGGTGCTTGGATCAGGAGCTTTTGGCACTGTCTACAAGGGCATC 2245
QY 652
Db 2246 TGGATCCAGATGGGAGAAATGTGAAAATCCCGTGGCTATCAAGGTGTTGAGAGAAAC 2305
QY 652
Db 2306 ACATCTCTAAAGCCAAAGAAATTTCTAGATGAAGCGTATGTGATGGTGTGGGT 2365
QY 652
Db 2366 TCTCCGTATGTGTCCCGCTCTCGGGCATCTGCGTGACATCCACAGTACAGCTGGTGACA 2425
QY 652
Db 2426 CAGCTTATGCCCTACGGCTGCCCTTCTGGACCATGTCCGAGAACACCGAGGTCCGCTTAGGC 2485
QY 652
Db 2486 TCCAGGACCTGTCAACTGGTGTGTTTCAGATTGCCAAGGGGATGAGTACTCTGGAGGAC 2545
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Db 2546 GTCCGGCTTGACACAGGGACCTGGCTGCCCGGAATGTGTAGTCAAGAGTCCCAACCAC 2605
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Db 2606 GTCAAGATTACAGATTTCCGGGCTGGCTCGGCTGCTGGACATTGTATGAGACAGAGTACCAT 2665
QY 652

Db 2666 GCAGATGGGGGCAAGGTGCCCATCAAAATGGATGGCATTTGGAATCTATTCTCAGACGCCGG 2725
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Db 2726 TTCAACCCATCAGAGTGTGTGGAGCTATGGAGTCACTGTGTGGAGCTGATGACTTTT 2785
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QY |||||SerGlnAsnGluAspLeuGlyProAlaSer
Db 663 ProLeuAspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuVal 682
QY |||||
Db 3026 CCCATGGACAGTACCTTTACCGTTCACTGTGTGGAAGATGATACATGGGTGACCTGGTA 3085
QY |||||
Db 683 AspAlaGluGlyTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGly 702
QY |||||
Db 3086 GACGCTGAAGATATCTGGTGGCCCCAGCAGGAGTTCTTCTCCCGGAGCCCTACCCAGGC 3145
QY |||||
QY 703 AlaGlyGlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAsp 722
Db 3146 ACTGGGACACAGCCCATAGAAAGCACCCGAGCTCTCCACAGGAGTGGAGGTGGTGGAG 3205
QY |||||
QY 723 LeuThrLeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSer 742
Db 3206 CTGACACTGGGCTGGAGCCCTCGGAAGAAAGGGCCCCCAGATCTCCACTGGCTCCCTCG 3265
QY |||||
Db 743 GluGlyAlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeu 762
QY |||||
Db 3266 GAAGGGCTGGCTCCGATGTTGATGGTACCTGGCAATGGGGGTAAACAAAGGGCTG 3325
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QY 763 GlnSerLeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrVal 782
Db 3326 CAGAGCTCTCTCCACATGACCTCAGCCCTCTACAGCGGTACAGCAGGAGCCACACATTA 3385
QY |||||
QY 783 ProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGlu 802
Db 3386 CCTCTCCCCCGGAGACTGATGGCTATGTTCCTCCCTGGCCTGCAGCCCCCAGCCGAG 3445
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QY 803 TyrValAsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuPro 822
Db 3446 TATGTGAACCAATCAGAGGTTCAAGCTCAGCCCTCTTAAACCCCGAGGGGTCTCTGCCT 3505
QY |||||
QY 823 AlaAlaProAlaGlyAlaThrLeuGluArgProIlyThrLeuSerProGlyLysAsn 842
Db 3506 CCTGTCCGGCTGCTGCTGCTACTCTAGAAAGAACCCCAAGACTCTCTCTCTGGGAAGAA 3565
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QY 843 GlyValIlyAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThr 862
Db 3566 GGGTGTGTCAAGACGCTTTTGGCTTCGGGGGTGCTGTGGAGAACCTGAAATCTTAGTA 3625
QY |||||
QY 863 ProGlnGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAsp 882
Db 3626 CCGAGAGAGGACATGCTCTCCGCCCCACCTCTCTCTCTGCTTCCAGCCAGCCTTTGAC 3685
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QY 883 AsnLeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLys 902
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QY 903 GlyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3746 GGGACCCCACTGCAGAGAACCTGTAGTACCTAGGCTGTGATGTACTGTGTA 3796

RESULT 15
US-08-645-865-14
; Sequence 14, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLU H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3955 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-645-865-14

Alignment Scores:
Pred. No.: 0 Length: 3955
Score: 4134.00 Matches: 781
Percent Similarity: 65.47% Conservative: 42
Best Local Similarity: 62.13% Mismatches: 96
Query Match: 81.41% Indels: 338
DB: 1 Gaps: 3

US-09-493-480-6 (1-919) x US-08-645-865-14 (1-3955)

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DB	26	ATGGAGCTGGCGCCTGGTGGCGCTGGGGGTTCCTCTCGCCCTCCTCGCCCGCCGGAATC	85
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
DB	86	GGGGGCCCAAGTGTGTACCGGCACAGACATGAAGTTCGGGCTCCCTGCCAGTCTTGAG	145
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValGlnGlyAsnLeu	60
DB	146	ACCCACCTGGACATGCTCCGCCACCTGTACACAGGCTGTGAGTAGTCAGGGCAACTTG	205
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80
DB	206	GAGCTTACCTAGTGGCTGCCAATGCCAGCTCTCATTCCTGAGGACATCCAGGAAGTT	265
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
DB	266	CAGGGTTACATGCTCTCTCACAACAGGTGAAGCGCTCCACTGCAAGAGCTGCGC	325
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120

DB	326	ATCGTGAGAGGACCCAGCTCTTTGAGGACAAAGTATGCCCTGGCTGTGTAGACAACCGA	385
QY	121	AspProLeuAsnAsnThrThrProValThr---GlyAlaSerProGlyGlyLeuArgGlu	139
DB	386	GATCCTCAGGCAATGTTCGCCCGCTCCACCCAGCAGAAACCCAGAGGGGTGCGGGAG	445
QY	140	LeuGlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnPro	159
DB	446	CTGACAGCTTCGAAGTCTCAGAGATCTCTGAAGGAGGAGTTTTCATCCGTGGGAACCT	505
QY	160	GlnLeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeu	179
DB	506	CAGCTCTGCTACGAGCATGGTTTGTGAAGGACGCTTCCGCAAGAAATAACCAACTG	565
QY	180	AlaLeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCys	199
DB	566	GCTCTGTCGATATAGACCAATCGTTCCCGGGCTGTCCACCTGTGCCCCCCTGTC	625
QY	200	LysGlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrVal	219
DB	626	AAAGCAATCACTGTTGGGGTGAGAGTCCGGAAGACTGTCTGACTCTTGACTGGCACCAC	285
QY	220	CysAlaGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGln	239
DB	686	TGTACCACTGGTGTGCGCGGTGCAAGGCGCGCTGCCACTGACTGTGCTGCATGAGCAG	745
QY	240	CysAlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsn	259
DB	746	TGTGCCGAGGCTGCACGGGCCCCAAGCATTTCTGACTGCTGGCTGCTCCCTCCTCAAT	805
QY	260	HisSerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPhe	279
DB	806	CATAGTGTATCTGTGAGCTGCACCTGCCAGCCCTCGTCACTACACACACACACCTTT	865
QY	280	GluSerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCys	299
DB	866	GAGTCCATGCACACCCCTGAGGCTCGCTACACCTTGGTGGCAGCTGGCTGACCACTGC	925
QY	300	ProTyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsn	319
DB	926	CCCTACAACTACCTGTCTACGGAAGTGGGATCTCTGCACTCTGGTGTGTCCCCCGGAAAC	985
QY	320	GlnGluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAla	339
DB	986	CAAGAGGTCAAGCTGAGGACGGAACACAGCGTTGTGAGAAATGACAGAACCTGTGCT	1045
QY	340	ArgValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAla	359
DB	1046	CGAGTGTCTATGCTGTGGCATGGAGCACCTTCCAGGGGGCGAGGGCCATCCACAGTGAC	1105
QY	360	AsnIleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGlu	379
DB	1106	AATGCCAGGAGTTGATGGCTGCAAGAAAGATCTTTGGGAGCTGGCATTTTTCGGGAG	1165
QY	380	SerPheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnVal	399
DB	1166	AGCTTTGATGGGACCCCTCTCCGGCATTTGCTCGCTGAGGCTGAGCAGCTCCAAGTG	1225
QY	400	PheGluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaThrProAspSerLeu	419
DB	1226	TTCCAAACCTCGGAGGAGATCACAGTTTACTGTATCATCTCAGCATGGCCAGACAGTCTC	1285
QY	420	ProAspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGly	439
DB	1286	CGTGACCTCAGTGTCTTCAGAACCTTCAATCATTCGGGGACGAGATCTCCACAGTGC	1345
QY	440	AlaTyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArg	459
DB	1346	GGGTACTATTGACACTGCAAGGCTGGGGATCCACTCGCTGGGGCTGCGCTCACTCGCG	1405
QY	460	GluLeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThr	479

Db 1406 GAGCTGGGCGAGTGAGTTGGCTCTGATTACCGGCAACGCCCATCTCTGCTTTGTACACACT 1465
Qy ValProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArg 499
Db 1466 GTACCTTTGGACACAGCTCTTTCCGGAACCCACATCAGGCCCTGTCTCCACAGCTGGGAACCGG 1525
Qy 500 ProGluAspGlu---CysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGly 518
Db 1526 CCGGAAGAGAGACTTGTGCGTCTCGAGCGGTGTGCTGTAACTCACTGTGTGCCACCGG 1585
Qy 519 HisCysTrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGln 538
Db 1586 CACTGTCTGGGGCCAGGCCCCACCCAGTGTGCTCACTGCGAGTCATTTCTTCGGGGCCAG 1645
Qy 539 GluCysValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArg 558
Db 1646 GAGTGTGTGGAGGAGTGCCGAGTATGGAAGGGGCTCCCGGAGTATGTGAGTGACAAG 1705
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QY	883	AsnLeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLys	902
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QY	903	GlyThrProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal	919
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Search completed: August 3, 2005, 12:58:29
 Job time : 522.375 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 3, 2005, 12:38:09 ; Search time 1373.71 Seconds
(without alignments)
4329.948 Million cell updates/sec

Title: US-09-493-480-6
Perfect score: 5078
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09493480 @CGN 1 1.1616 @runat_02082005_152648_25157
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4900	96.5	3768	9	US-09-765-973-1
2	4900	96.5	3768	9	US-09-854-356-9
3	4900	96.5	3768	9	US-09-930-125-1
4	4900	96.5	3768	16	US-10-313-644-1
5	4900	96.5	4473	10	US-09-441-411-5
6	4900	96.5	4473	15	US-10-146-473-32
7	4900	96.5	4473	15	US-10-207-655-44
8	4900	96.5	4473	15	US-10-101-510-81
9	4900	96.5	4473	20	US-10-762-128-5
10	4900	96.5	4473	20	US-10-723-860-8
11	4892	96.3	3768	9	US-10-207-498-5
12	4892	96.3	3768	9	US-09-811-123-8
13	4892	96.3	3768	9	US-09-811-115-2
14	4892	96.3	3768	11	US-09-984-092-3
15	4892	96.3	3768	18	US-10-280-576-3
16	4892	96.3	3768	19	US-10-441-779C-3
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18	4892	96.3	4530	9	US-09-877-177-11
19	4892	96.3	4530	15	US-10-177-293-125
20	4892	96.3	4530	15	US-10-007-926A-119
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33	4892	96.3	4530	21	US-10-928-465-75
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37	4892	96.3	4642	14	US-10-198-846-10896
38	4892	96.3	9274	9	US-09-811-123-7
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42	4849	95.5	4543	9	US-09-769-508-1
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44	4434.5	87.3	3504	21	US-10-794-514A-329
45	4232.5	83.3	3564	21	US-10-794-514A-331

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09765973
; Publication No. US20020039573A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmermann, Susan
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND
; TREATMENT OF HER-2/neu ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.496
; CURRENT APPLICATION NUMBER: US/09/765,973
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768

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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-765-973-1

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 9 Gaps: 1

US-09-493-480-6 (1-919) x US-09-765-973-1 (1-3768)

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Db 3061 GAGGAGTATCTGTACCCAGCAGGCTTCTTCTGTCCAGACCTTGCCTGGGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCATGGTCCACCACAGGACCGCAGCTCATCTACCAGGAGTGGCGTGGGAGCCTGACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGCTGGAGCCCTCTGAAGAGGAGGCCCTCCAGGTCTCCACTGGCACCTTCGAAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGGTACCTGGGAATGGGGACGCCAAGGGGCTGCAAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCACACATGACCCCGACCTCTACAGCGGTACAGTGAGGACCCACAGTACCCCTG 3360
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCTCTGAGACTGATGGCTACGTTGCCCTCCCTGACCTGCAGCCCCCAGCTGATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCAGCAGATGTTCCGGCCCCCAGCCCCCTTCCGCCGAGAGGGCCCTCTGCTGCTGCC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGGTGCCACTCTGGAAGAGGCCCAAGACTCTCTCCCGAGGGAAGAATGGGGTC 3540
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGAGCGTTTTTGGCTTTGGGGTGGCGTGAGAACCCCGAGTACTTTGACACCCAG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGTGGCCCTCAGCCCCCAGCCCCCTCTCTGCTGCTTCCAGCCAGCGCTTCGACACCTC 3660
Qy 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACCGAGCCACCCAGAGCGGGGGCTCCACCCAGCACCTTCAAAGGAGCA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3765

RESULT 2

US-09-854-356-9
; Sequence 9, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens

Db 1741 GCTGACAGTGTGGGCTGTGCCACTATAAGACCTCCCTTCTGCGTGGCCGCTGC 1800
Qy 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
Db 1801 CCACGGGTGTGAACCTGACCTCTCTCATATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db 1861 GGGGCATGCCAGCCTTGGCCCATCACTGCACCCACTCTCTGTGTGGACCTGGATGACAA 1920
Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGCTGCCCCCGCAGCAGAGAGCCGCTCTGACGTCCATCATCTCTGCGGTGTGGC 1980
Qy 653 ----- 653
Db 1981 ATTCTGCTGCTGCTGTGGGCTGTCTTTGGGATCCTCATCAAGCAGCGCAGCAG 2040
Qy 653 ----- 653
Db 2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2100
Qy 653 ----- 653
Db 2101 ACACCTAGCGAGCGATGCCCAACAGCGCAGATCGGATCCTGAAAGAGACGGAGCTG 2160
Qy 653 ----- 653
Db 2161 AGAAGGTGAAGTGTGGATCTGGGCGCTTTTGGCACAGTCTACAAGGCATCTGGATC 2220
Qy 653 ----- 653
Db 2221 CCTGATGGGAGAATGTGAAATTTCCAGTGGCCATCAAAAGTTGTAGGGAAACACATCC 2280
Qy 653 ----- 653
Db 2281 CCCAAAGCCAAAGAAATCTTAGAGAAAGCATACGTGATGCTGTGGTGTGGCTCCCCA 2340
Qy 653 ----- 653
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Qy 653 ----- 653
Db 2401 ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAACCGCGACGCTGGCTCCAG 2460
Qy 653 ----- 653
Db 2461 GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGGATGAGTACTCTGGAGGATGTGCGG 2520
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Db 2521 CTCGTACACAGGACTTGGCCGCTCGGAACGTGCTGTGAAGAGTCCCAACCATGTCAAA 2580
Qy 653 ----- 653
Db 2581 ATTACAGACTTTCGGGCTGGCTCGGCTGCTGGACATTGAACAGACAGAGTACCATGCAGAT 2640
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Db 2641 GGGGGCAAGTGGCCATCAAGTGGATGGCGCTGGAGTCCATTTCTCCGCGCGGTTCAAC 2700
Qy 653 ----- 653
Db 2701 CACCAGATGATGTGGAGTTATGGTGTACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
Qy 653 ----- 653
Db 2761 AAACCTTACGATGGATCCCGAGCCCGGGAGATCCCTGACCTGTGGAAAGGGGAGCGG 2820
Qy 653 ----- 653

Db 2821 CTGCCCCAGCCCCCATCTGCAACCATTTGATGTCTCATATGATCATGTGTCAAATTTGTGGATG 2880
Qy 653 ----- 653
Db 2881 ATTGACTCTGAATGTTCGGCCCAAGATTCCGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGAGCGCTTTGTGGTTCATCCAGAAATGAGGACTTGGGCGCCAGCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGACCTTCTTACCGCTACCTGCTGGAGAGCATGACATGGGGACCTCTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTTACCCAGCAGGCTTCTTCTGTCCAGACCTTGCCTCCGGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3121 GGCATGGTCCACACAGCAGCCAGCTCATCTACCAGGAGTGGCGTGGGACCTGCACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCCCCAGGTCTCCACTGGCACCCTCCGAAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGGTACCTGGGATGGGGCAGCCAGGGGCTGCAAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCACACATGACCCAGCCCTCTACAGCGGTACAGTGAGGACCCACAGTACCCTG 3360
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCTCTGAGACTGATGGTACGTTCGCCCTTACCTGACGCCCCAGCCTGAATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCAGCAGATGTTCCGGCCCGCAGCCCTTTCGCCCGAGAGGGCCCTCTGCTGCTGCC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGGTGCCACTCTGGAAGGCCCAAGACTCTCTCCCGAGGGAAGATGGGGTC 3540
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGAGCGTTTTTTCCTTTGGGGGTGGCGTGGAGAACCCCGAGTACTTGCACACCCAG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCCCTCAGCCCGCAGCCCTCTCTCTGCTTCCAGCCAGCCTTCGACCACTC 3660
Qy 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACCGAGCCACCCAGAGCGGGGGCTCCACCCAGCAGCTTCAAAGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAAACCCAGAGTACTTGGGTCTGGAGCTGCCAGTG 3765

RESULT 3

US-09-930-125-1

; Sequence 1, Application US/09930125

; Publication No. US20020193329A1

; GENERAL INFORMATION:

; APPLICANT: Hand-Zimmerman, Susan

; APPLICANT: Cheever, Martin A.

; APPLICANT: Foy, Teresa M.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Kalos, Michael D.

; APPLICANT: McNeill, Patricia D.

APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.544
CURRENT APPLICATION NUMBER: US/09/930.125
CURRENT FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3768
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(3765)
US-09-930-125-1

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 9 Gaps: 1

US-09-493-480-6 (1-919) x US-09-930-125-1 (1-3768)

QY	1	MetGluLeuAlaLeuAlaLeuCysArgTrrGlyLeuLeuLeuAlaLeuLeuProGlyAla	20
DB	1	ATGGAGCTGGGGCCTTGTGGCGCTGGGGCTCCTCTCGCCCTCTTGGCCCCCGGAGCC	60
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
DB	61	GGGAGACCAAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCTCGCCAGTCCCGAG	120
QY	41	ThrHisLeuAspMetLeuArgHisLeuYrGlnGlyCysGlnValValGlnGlyAsnLeu	60
DB	121	ACCCACCTGGACATGCTCCGCCACCTCTACAGGGCTGCGAGGTGGTGGTGGAGAACCTG	180
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80
DB	181	GAACCTCACCTAGCTGCCACCAATGCCAGCTGTCTCTCGAGGATATCCAGAGAGTG	240
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
DB	241	CAGGGCTAGTGTCTATCGCTCACAACCAAGTGAGGCAGGTCCACTGCAGAGGCTGCG	300
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
DB	301	ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGACAATGA	360
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
DB	361	GACCCGCTGAACAATACCACTCTGTACAGAGGGCTCCCGAGAGGCTCGGGAGCTG	420
QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
DB	421	CAGCTTCGAAGCTCACAGAGATCTTGAAGGAGGGGTCTTGTATCCAGGGGAACCCCG	480
QY	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
DB	481	CTCTGTACAGACACGATTTTGTGAAGGACATCTTCCACAAGAACCAACAGCTGGCT	540
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	541	CTCACACTATAGACACCAACCGCTCTCGGGCTGCCACCTGTCTCCGATGTGTAA	600
QY	201	GlySerArgCysTrpGlyGluSerGluAspCysGlnSerLeuThrArgThrValCys	220
DB	601	GGCTCCCGCTGTGGGAGAGAGTCTGAGGATTTGTAGAGCTGTACAGGCTGTACGGCT	660
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysHisGlnGlnCys	240

DB	661	GCCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCCACTGCTGCTGCCACTGAGCAGTGT	720
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	721	GCTGCCGGCTGCACGGGCCCAAGCACTGTGACTGCTGGCTGCTCCTCCTCAACCCAC	780
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
DB	781	AGTGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACTACACACAGACAGCTTTGAG	840
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
DB	841	TCCATGCCCAATCCCGAGGGCGGTATACATTCGGCGCCAGCTGTGTGACTGCTGTGCC	900
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	901	TACAACTACCTTTCTACGGACGTGGGATCCTGCACCTCTGCTGCCCTGTCACACCA	960
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
DB	961	GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAGTGCAGCAGCCCTGTGCCCA	1020
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1021	GTGTCTATGTCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACCACTGCGCAAT	1080
QY	361	IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1081	ATCCAGGAGTTTGTGGCTGCAAGAGATCTTTGGAGCCTGGCATTTCTGCCGAGAGC	1140
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe	400
DB	1141	TTTGATGGGACCCAGCCTCCAACTGCCCCGCTCCAGCCAGAGCAGCTCCAGTGT	1200
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuYrIleSerAlaTrpProAspSerLeuPro	420
DB	1201	CAGACTCTGGAAGAGATCACAGTTTACCTATATACATCTCAGCATGCGCGGACAGCT	1260
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	1261	GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGACAGAAATCTGCACAAATG	1320
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1321	TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGCTGGGGCTGCGCTCACTGAGGAA	1380
QY	461	LeuGlySerGlyLeuAlaIleIleHisAsnThrHisLeuCysPheValHisThrVal	480
DB	1381	CTGGGACGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTGTGCACACGG	1440
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	1441	CCCTGGGACCACTCTTTCGGAAACCCGACCCAGCTTGTCTCCACTGCCAACCGGCCA	1500
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	1501	GAGGACGAGTGTGTGGCGAGGGCTGGCTGCCACACAGCTGTGCGCCCGGCGACCTGC	1560
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	1561	TGGGTCCAGGGGCCCAACCCAGTGTCACTGACAGCTGTCAGTACCTGTTTTGGACCG	1620
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
DB	1621	GTGGAGGAATCCCGAGTACTGCGAGGGCTTCCCGAGGAGTATGTGATGCCAGGCACT	1680
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	1681	TTGCCGTGCCACCTGTAGTGTGAGCCCAAGATGCTCAGTACCTGTTTTGGACCGGAG	1740
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
DB	1741	GCTGACCAAGTGTGGCTGTGCCCACTATAAGGACCTTCCCTTCTGCGTGGCCCGCTGC	1800

Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
Db	1801	CCCAGCGTGTGAACCTGCCTCTCCTACATGCCCATCTGGAAGTTTCAGATGAGGAG	1860
Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValaspLeuAspAspLys	640
Db	1861	GGCGATGCCAGCCTTGCCCCATCACTGCACCCACCTCCTGTGTGGACCTGGATGACAAG	1920
Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	1921	GGCTGCCCGCCGAGCAGAGAGCCAGCCCTCTGACGTTCCATCATCTCTCGCGTGTGGC	1980
Qy	653	-----	653
Db	1981	ATTCTGCTGTCGTGTGTCCTTTGGGGTGGTCTTTGGGATCTCTCATCAAGCGACGCGACAG	2040
Qy	653	-----	653
Db	2041	AAGATCCGGAAGTACACGATCGCGAGACTGCTGCAGGAAACGGAGCTGTGTGGAGCCGCTG	2100
Qy	653	-----	653
Db	2101	ACACTAGCGGAGCGATGCCCAACCGCGCAGATCGGATCTCTGAAGAGACGGAGCTG	2160
Qy	653	-----	653
Db	2161	AGGAAGGTGAAGTCTTGGATCTGGGCTTTTGGCACAGTCTACAAGGCGATCTGGATC	2220
Qy	653	-----	653
Db	2221	CCTGATGGGAGAAATGTGAANAATTCAGTGGCCATCAAAGTGTGTGAGGGAACACATCC	2280
Qy	653	-----	653
Db	2281	CCCAAGCCAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGCTCCCCA	2340
Qy	653	-----	653
Db	2341	TATGTCTCCGCGCTTCTGGGCACTGCTGCATCCACGCTGCAGCTGTGACACAGCTT	2400
Qy	653	-----	653
Db	2401	ATGCCCTATGGCTGCCCTTTAGACCATGTCGGGAAACCGCGGACGCCCTGGGCTCCCAG	2460
Qy	653	-----	653
Db	2461	GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGATGAGTACTCTGGAGGATGTCCGG	2520
Qy	653	-----	653
Db	2521	CTCGTACACAGGGACTTGGCGGCTCGGAACGTGTGTCGAAGAGTCCCAACCATGTCAAA	2580
Qy	653	-----	653
Db	2581	ATTACAGACTTCGGGCTGGCTCGCTGCTGGACATTGACGAGACAGAGTACCATGCAGAT	2640
Qy	653	-----	653
Db	2641	GGGGCAAGTGCACATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGCGGTTCAACC	2700
Qy	653	-----	653
Db	2701	CACCAGAGTGATGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC	2760
Qy	653	-----	653
Db	2761	AAACCTTACGATGGATCCACAGCCCGGAGATCCCTGACCTGCTGGGAAGGGGAGCGG	2820
Qy	653	-----	653
Db	2821	CTGCCCGAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAAATGTTGGATG	2880

Qy	653	-----	653
Db	2881	ATTGACTCTGAATGTGCGCCAAAGATTTCGGAGAGTTGGTGTCTGAATCTCCCGCATGGCC	2940
Qy	654	-----	664
Db	2941	AGGGACCCCGCCGCTTTGTGGTTCATCCAGAAATGAGGACTTTGGCCCGCAGCCAGTCCCTTG	3000
Qy	665	AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla	684
Db	3001	GACAGCACCTTCTACCGCTCACTGCTGGAGAGCGATGACATGGGGGACCTGGTGGATGCT	3060
Qy	685	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	704
Db	3061	GAGAGATATCTGGTACCCACGAGGGCTTCTTGTCACAGCCCTGCCCGGGCGCTGGG	3120
Qy	705	GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr	724
Db	3121	GGCATGTGTCACACAGGCACCCGAGCTCATCTACAGGAGTGGCGTGGGACCTGACA	3180
Qy	725	LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly	744
Db	3181	CTAGGGCTGGAGCCCTCTGAAGAGAGAGCCCCAGAGTCTCACTGGGCACCCCTCCGAAGGG	3240
Qy	745	AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaIysGlyLeuGlnSer	764
Db	3241	GCTGGCTCCAGTATTTGATGTGACTGGGAATGGGGGACGCCAAGGGGCTCGAAAGC	3300
Qy	765	LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu	784
Db	3301	CTCCCCACATGACCCCGACCCCTCTACAGCGGTACAGTGAGGAGCCCAAGTACCCCTG	3360
Qy	785	ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal	804
Db	3361	CCCTCTGAGACTGATGGCTAGTTGGTCCCCCTGACCTGCAGCCCCCAGCCTGAATATGTG	3420
Qy	805	AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla	824
Db	3421	AACCAGCCAGATGTTGGGCCCCAGCCCTTCGCCCCCGAGAGGGCCCTCTGCCTGTCTGC	3480
Qy	825	ArgProAlaGlyAlaThrLeuGluArgProGlyThrLeuSerProGlyIysAsnGlyVal	844
Db	3481	CGACCTGCTGGTGCCACTCTGSAAGAGGCCCAAGACTCTCTCCCCAGGAAGAATGGGGCT	3540
Qy	845	ValIysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln	864
Db	3541	GTCAAGACCGTTTTTGGCTTTGGGGGTGCGGTGGAGNACCCCGAGTACTTTGACACCCCG	3600
Qy	865	GlyCylAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu	884
Db	3601	GGAGGGAGCTGCCCTCTCAGCCCCACCTCTCTCTCTGCGCTTCAGCCCGCAGCTTCG	3660
Qy	885	TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheIysGlyThr	904
Db	3661	TATTACTGGGACCCAGNACCCACAGAGCGGGGGGCTCCACCCAGACCTTCAAGGGACA	3720
Qy	905	ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal	919
Db	3721	CCTACGGCAGAGAACCCAGAGTACCTGGGTCTGGAGCTGCCAGTG	3765

RESULT 4
US-10-313-644-1
; Sequence 1, Application US/10313644
; Publication No. US20030157119A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmerman, Susan
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.483C3
; CURRENT APPLICATION NUMBER: US/10/313,644
; CURRENT FILING DATE: 2002-12-04

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-313-644-1

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservatives: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 336 Indels: 336
DB: 16 Gaps: 1

US-09-493-480-6 (1-919) x US-10-313-644-1 (1-3768)

QY 1 MetGluLeuAlaLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
DB 1 ATGGAGCTGGCGGCTTGTGGCGCTGGGGGCTCTCTCGCCCTCTGTGCCCCCGAGGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 61 GCGAGCACCAGTGTGCACCGGCACAGACATGAAGCTGGGCTCTCTGCCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrgingGlyCysGlnValValGlnGlyAsnLeu 60
DB 121 ACCCACCTGGACATGCTCCGCCACCTCTACCAAGGCTGCGAGGTGCGAGGAAACCTG 180
QY 61 GluLeuThrTyrlProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
DB 181 GAACTCACCTAGCTGCTCCCAACCAATGCCAGCTGTCTCTCGAGGATATCCAGAGGTG 240
QY 81 GlnGlyTyrlValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 241 CAGGGCTAGTGTCTCTCTCAACCAAGTGAAGGAGGTCTCCACTGACAGAGGTGGG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrlAlaLeuAlaValLeuAspAsnGly 120
DB 301 ATTGTGCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCGGTGTAGACATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 361 GACCCGCTGAACAATACCAACCCCTGTCAAGGGGCTCCCAAGGAGGCTGCGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValValLeuIleGlnArgAsnProGln 160
DB 421 CAGCTTCGAAGGCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCA 480
QY 161 LeuCysTyrlGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
DB 481 CTCTGTACAGGACACAGATTTTGTGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTTGCACCCCTGTCTCCGATGTGTAA 600
QY 201 GlySerArgCysTrpGlyGluSerGluAspCysGlnSerLeuThrArgThrValCys 220
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QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysHisGlnGlnCys 240
DB 661 GCCGGTGGCTGTGCCGCTGCAAGGGCCACTGCCCACTGCTGTGCTGCTGCTGCTGCTG 720
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281 SerMetProAsnProGluGlyArgTyrlThrPheGlyAlaSerCysValThrAlaCysPro 300
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301 TyrlAsnTyrlLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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Qy 885 TrrTrrAspGlnAspProProGluArgGlyAlaProSerThrPheLysGlyThr 904
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RESULT 5
US-09-441-411-5
; Sequence 5, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-441-411-5

Alignment Scores:

Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 10 Gaps: 1

US-09-493-480-6 (1-919) x US-09-441-411-5 (1-4473)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
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QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
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QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
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RESULT 6
US-10-146-473-32
; Sequence 32, Application US/10146473
; Publication No. US2003010888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
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Score:

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US-09-493-480-6 (1-919) x US-10-146-473-32 (1-4473)							
QY	1	MetGluLeuAlaAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProProGlyAla	20	Db	1135	GAGGTGCACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA	1194
Db	175	ATGGAGCTGGCGCCTTGTGCGCTGGGGCTCCTCTCGCCCTTTGCCCGGAGCC	234	QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40	Db	1195	GTGTCTATGTCTTGGGCATGGAGCACATTTCGAGAGGTGAGGCGAGTTACCAAGTGC	1254
Db	235	GGGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGGGGCTCCCTGCCAGTCCCGAG	294	QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60	Db	1255	ATCCAGAGGATTGTCTGGCTGCAAGAAGATCTTTGGAGCGCTGGCATTTCTGCCGAGAGC	1314
Db	295	ACCCACCTGGACATGCTCGGCCACCTCTACCAAGGCTGCCAGGTGTGTGAGGGAACCTG	354	QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80	Db	1315	TTTGATGGGAGCCAGCCCTCCAAACATGCTCCCGCTCCAGCCAGAGCAGCTCCCAAGTGT	1374
Db	355	GAACTCACCTACTGCTGCCCAACCAATGCCAGCCTGTCTCTTCCTGCAGGATATCCAGGAGTG	414	QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTTPProAspSerLeuPro	420
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100	Db	1375	GAGACTCTGGAAGAGATCACAGGTTTACCTATACATCTCAGCATGCGCGGACAGCCTGCCT	1434
Db	415	CAGGGCTACGTCTCATCTCACAACCAAGTGAGGAGGCTCCCACTGCAGAGGCTGGCG	474	QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120	Db	1435	GACCTCAGCGTCTTCCAGNAACCTGCAGTAATCCGGGAGAGAAATCTGCACAATGGCGCC	1494
Db	475	ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCGCTGGCGGTGTGACACAATGGA	534	QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTTPLeuGlyLeuArgSerLeuArgGlu	460
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140	Db	1495	TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCACTGAGGGAA	1554
Db	535	GACCCGCTGAACATACCAACCCCTGTTCACAGGGGCTTCCCAAGAGGCTGCGGAGCTG	594	QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
QY	141	GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuIleGlnArgAsnProGln	160	Db	1555	CTGGCAGTGGACTGGCCCTCATCCACCAATAACCCACCTCTGCTTGTGTGCACACGGTG	1614
Db	595	CAGCTTCGAAGCCTCACAGAGATCTTTGAAGAGGGGTCTTGATCCAGCGGAACCCCCAG	654	QY	481	ProTTPAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
QY	161	LeuCysTyrGlnAspThrIleLeuThrLysAspIlePheHisLysAsnGlnLeuAla	180	Db	1615	CCCTGGGACCAGCTCTTTCCGGAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1674
Db	655	CTCTGTCTACAGAGACACGATTTTGTGGAAGGACATCTTCCACAAGAACCAACAGCTGGCT	714	QY	501	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200	Db	1675	GAGGACGAGTGTGTGGCGAGGGCTGGCTGCCACCACTGTCGCGCCGAGGGCACTGC	1734
Db	715	CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAAG	774	QY	521	TTPGlyProGlyProThrGlnCysValaAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
QY	201	GlySerArgCysTTPGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220	Db	1735	TGGGTTCAGGGCCACCAGTGTCTCACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC	1794
Db	775	GGCTCCCGTGTGGGAGAGAGTTCTGAGGATTGTGAGAGCTGCAGCGCCTGCTCTGT	834	QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValaAsnAlaArgHisCys	560
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240	Db	1795	GTGGAGGAATGCCAGTACTGCAGGGCTTCCCGGAGGATGTGTAATGCCAGGCACCTGT	1854
Db	835	GCCGTTGGTGTGCCCGCTGCAAGGGGCCACTGCCCACTGACTGTGCCATGAGCAGTGT	894	QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260	Db	1855	TTGCCGTGCCACCCCTGAGTGTGAGTGTGAGCCCAAGAAATGGCTCAGTGACCTGTTTGGACCGGAG	1914
Db	895	GCTGCCGCTGCACGGGCCCAAGCACTCTGACTGCTGGCTGGCTGCCATCTCAACCA	954	QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys	600
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	Db	1915	GCTGACCAAGTGTGGCTGTGCCACTATAGAGACCTTCCCTTCTGCGTGGCCCGCTGC	1974
Db	955	AGTGGCATCTGTGAGTGACTGCCAGCCCTGGTCACTACACACAGACACGTTTGAG	1014	QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTTPLeuPheProAspGluGlu	620
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300	Db	1975	CCACGGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	2034
Db	1015	TCCATGCCCAATCCCGAGGGCGGTATACATTCGGCGCCAGCTGTGTGACTGCCCTGTGCC	1074	QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValaAspLeuAspAspLys	640
QY	301	TyrAsnThrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	Db	2035	GGCGCATGCCAGCCTTGGCCCATCAACTGACACCCCACTCTCTGTGTGGACCTGSGATGACAAAG	2094
Db	1075	TACAACTACTTCTACGACGCTGGGATCTTGACACCTCTGTCTGCCCGCCAGCTGTG	1134	QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	Db	2095	GGCTGCCCGCCGACAGAGACCCCTCTGACGTCCATCATCTCTCGCGTGGTGGC	2154
				QY	653	-----	653
				Db	2155	ATTCTGCTGGTGTGGGTCTTGGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG	2214
				QY	653	-----	653
				Db	2215	AAGATCCGGAAGTACACGATGCGGAGACTGTGTGAGGAAACGGAGCTGTGTGGAGCCGCTG	2274


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QY 653 ----- 653
Db 2275 ACACCTAGCGGCGATGCCAACACAGCGCAGATCGGATCCTGAAAGACGGAGCTG 2334
QY 653 ----- 653
Db 2335 AGGAAGTGAAGTGCTTGATCTGGCGTTTGGCACAGCTACAAAGGCGATCTGGATC 2394
QY 653 ----- 653
Db 2395 CCTGATGGGAGAAATGTGAAATTTCCAGTGGCCATCAAAGTGTGAGGAAACACATCC 2454
QY 653 ----- 653
Db 2455 CCCAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGCTGTGTGGGCTCCCCA 2514
QY 653 ----- 653
Db 2515 TATGTCTCCGCGCTTCTGGGCACTCTGCGCATCTGCGTGACATCCACGGTGAGCTGTGACACAGCTT 2574
QY 653 ----- 653
Db 2575 ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAAAACCGCGGACGCGCTGGGCTCCAG 2634
QY 653 ----- 653
Db 2635 GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGATGAGCTACCTGGAGGATGTGCGG 2694
QY 653 ----- 653
Db 2695 CTCGTACACAGGACTTGGCGGCTCGGAACGTCTGCTCAAGAGTCCCAACCATGTCAAA 2754
QY 653 ----- 653
Db 2755 ATTACAGACTTCGGGTGGCTCGGCTGCTGGACATTGACGAGACAGATACCATGAGAT 2814
QY 653 ----- 653
Db 2815 GGGGCAAGTGGCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGCTTCAAC 2874
QY 653 ----- 653
Db 2875 CACCAGATGATGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934
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Db 2935 AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGTGAAAAGGGGAGCGG 2994
QY 653 ----- 653
Db 2995 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTCAAATGTTGGATG 3054
QY 653 ----- 653
Db 3055 ATTGACTCTGAATGTCCGCCAAGATTCGGGAGTTGGTGTCTGAATTTCTCCCGATGGCC 3114
QY 654 -----GlnAsnGluAspLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3115 AGGGACCCCGCGCTTTGTGTCTCCAGATGAGACTTTGGGCCAGCCAGCTCCCTTG 3174
QY 665 AppSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGTGTGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTATACCCAGCAGGCGCTTCTTGTCCAGACCTGCCCGCGCGCTGGG 3294
QY 705 GlyMetValHisIleArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3295 GGCAATGTCACACAGGACCCAGCTCATCTACCAGGAGTGGCGGTGGGGACCTTGACA 3354
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QY 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGCGCTGGAGCCCTCTGAAGAGGAGGCCCCAGGCTCTCCACTGGCACCTCCGAAGG 3414
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyLeuGlnSer 764
Db 3415 GCTGGCTCGATGTATTTGATGTGACCTGGGANTGGGGCAGCCCAAGGGGCTGCAAAGC 3474
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3475 CTCCCCACACATGACCCCGCCCTCTACAGCGGTACAGTGAGGACCCACAGTACCCCTG 3534
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCTCTGAGACTGATGGCTACGTTGCCCGCTGACCTGCAGCCCCCAGCCCTGAATATGTG 3594
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACCAAGCCAGATGTTCCGCCCCAGCCCTTTCGCCCGAGAGGGCCCTCTGCCCTGTGCC 3654
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGCTGGTGCCTACTCTGGAAGGCCCAAGACTCTCTCCCGAGGAAGATGGGGTC 3714
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAGAGCGTTTTCCTTGGGGGTGGCTGGAGAACCCCGAGTACTTTGACACCCAG 3774
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGCTGCCCTCAGCCCGCCCTCTCTCTGCTTTCAGCCAGCTTTCGACAACTC 3834
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGGACGAGCCACCAGAGCGGGGCTCCACCCAGCACCTTCAAGGAGGACA 3894
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGGCAGAAACCCAGAGTACCTGGGTCTGGAGTGCCAGTG 3939

RESULT 7
US-10-207-655-44
; Sequence 44, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-207-655-44

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 15 Gaps: 1

US-09-493-480-6 (1-919) x US-10-207-655-44 (1-4473)

QY 1 MetGluLeuAlaAlaLeuCysArgTTPGlyLeuLeuAlaLeuLeuProGlyAla 20
Db 175 ATGGAGCTGGCGGCTTTGTGGCGCTGGGGCTCTCTCTGCGCTCTTGGCCCCCGGAGCC 234
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QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40		1315	TTTGTATGGGACCCAGCCTCCAAACAGTGCCTCCAGCCAGAGCAGCTCCAAGTGT	1374
DB	235	GGGAGACCAAGTGTGCACCGGCACAGACATGAGTCTGGGCTCCTCCAGTCCCGAG	294				
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60		401	GluThrLeuGluGluLeuThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro	420
DB	295	ACCCACCTGGACATGCTCCGCCACCTCTACACAGGGCTGCAGGTGTGCAGGAAACCTG	354		1375	GAGACTCTGGAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGACAGCTGCCT	1434
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80		421	AspLeuSerValPheGlnAsnLeuGlnValIleLeuArgGlyArgIleLeuHisAsnGlyAla	440
DB	355	GAACCTACACTAGTCTGCCACCAATGCCAGCCCTGCTCTCTCGAGGATATCCAGAGGTG	414		1435	GACCTCAGGCTTTCAGAACTGCAGATTAATCCGGGGACGAATTCCTGCACATGGCGGC	1494
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100		441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu	460
DB	415	CAGGGCTACGTCTCATCTCCTCACAACCAAGTGAGGCAGTCCCACCTGCAGAGGCTGCGG	474		1495	TACTCGTGACCTGCAGGGCTGGGCATCAGCTGGCTGGGGCTGCCTCACTAGGGAA	1554
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120		461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
DB	475	ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGACAATGGA	534		1555	CTGGGCAGTGGACTGGCCCTCATCCACCATAAACACCCACCTCTGCTTCGTGCACACGGTG	1614
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140		481	ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	535	GACCCGCTGAACAATACCAACCCCTGTCAAGGGGCTCCCGAGGAGCCCTGGCGGAGCTG	594		1615	CCCTGGGACCAGCTCTTTCGGAAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1674
QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160		501	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	595	CAGCTTCGAAGCTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCCAG	654		1675	GAGGACGAGTGTGGCGAGGGCTGGCTGCCACCACTGTGGCCCGAGGGCACTGC	1734
QY	161	LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLeuAsnAsnGlnLeuAla	180		521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	655	CTCTGTACAGGACACGATTTTGTGGAAGGACATCTTCACAAGAACCAACAGCTGGCT	714		1735	TGGGTCCAGGGCCACCCAGTGTGTCACTGCACCCAGTTCCTTCGGGGCCAGGAGTGC	1794
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200		541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
DB	715	CTCACACTATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGTAA	774		1795	GTGGAGGAATGCCGAGTACTGCAGGGGTCTCCACAGGAGATGTGAAATGCCAGGCACTGT	1854
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220		561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	775	GGCTCCCGCTGTGGGAGAGATTCGAGGATTTGTACAGGCTGCAGCGCTGCTCTGT	834		1855	TTGCGCTGCCACCTGAGTGTGAGCCCAAGATGCTCAGTGCACCTGTTTGGACCGGAG	1914
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240		581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
DB	835	GCCGCTGGCTGTGCCGCTGCAAGGGCCACTGCCCACTGCTGCTGCCATGAGCAGTGT	894		1915	GCTGACCACTGTGGCTGTGCCCACTATAAGGACCTCTCTGCTGCGTCCCGCTGC	1974
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260		601	ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu	620
DB	895	GCTGCCGCTGCAGGGGCCCAAGCACTCTGACTGCTGGCTGCCCTCCACTTCACACAC	954		1975	CCACGCGTGTGAACCTGACCTCTCTACATGCCCACTCTGGAAGTTTCCAGATGAGGAG	2034
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280		621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
DB	955	AGTGGCATCTGTGAGCTGCCACTGCCAGCCCTGGTCACCTACAAACACACACACGTTTGAG	1014		2035	GGCGCATGCCACCTTGCCCATCAACTCACTGCACCCACTCTCTGTGTGGACCTGTGATGACAAG	2094
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300		641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
DB	1015	TCCATGCCCAATCCCGAGGCGCGGTATACATTCGGCGCCAGCTGTGTGACTGCCTGTCCC	1074		2095	GGTCCCCCGCGAGAGAGAGCCCTCTGACGTCCATCATCTCTCGGTGTGTGGC	2154
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320		653	-----	653
DB	1075	TACAACTACTCTTCTACGAGCGTGGATCTCTGACCCCTCGTCTGCCCTCCCTGCACAAACAA	1134		2155	ATTCTGCTGCTGCTGCTTGGGGTGTCTTTGGGATCCTCATCAAGCAGCGGCAGCAG	2214
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340		653	-----	653
DB	1135	GAGGTGACAGCAGAGGATGGACACACAGCGGTGTGAGAAAGTGCAGCAAGCCCTGTGCCCGA	1194		2215	AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGAGCTGTGTGGAGCCGCTG	2274
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360		653	-----	653
DB	1195	GTGTGCTATGTGCTGGGCATGGAGCACTTGCAGAGGTGAGGCGAGTTACCAGTGCCTAAT	1254		2275	ACACCTAGCGGAGCGATGCCCAACCGCGCGAGATGCGGATCCTGAAAGAGACGGAGCTG	2334
QY	361	IleGlnGluPheAlaGlyCysLysValIlePheGlySerLeuAlaPheLeuProGluSer	380		653	-----	653
DB	1255	ATCCAGAGTGTCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGC	1314		2335	AGGAAGGTGAAGTGTCTTGGATCTGGCGTCTTTGGCACAGTCTACAGGGCATCTGGATC	2394
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400		653	-----	653

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QY 653 -----
Db 2455 CCCAAAGCCAAACAAAGAAATCTTAGAGAGACATACGTGATGGCTGGTGGGCTCCCCA 2514
QY 653 -----
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QY 653 -----
Db 2575 ATGCCCTATGGCTGCCCTTTAGACCATGTCCGGGAAAAACCGCGGACGCTGGGCTCCAG 2634
QY 653 -----
Db 2635 GACCTGTGTAAGTGGTGTATGCAGATTGCCAAGGGATGAGCTACCTGGAGGATGTCCGG 2694
QY 653 -----
Db 2695 CTCGTACACAGGACTTGGCCGCTCGGAACGTGCTGTCAGAGTCCCAACCATGTCAAA 2754
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QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGGACCCCGAGCGCTTTGTGGTCAATCCAGAAATGAGGACTTGGGCCCGACGATCCCTTG 3174
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGACCTTTCTACCGCTCACTGTGGAGACGATGACATGGGGACCTGGTGGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTTACCCAGCAGGGGCTTCTCTGTCCAGACCTGCCCCGGCGCTGGG 3294
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3295 GGATGGTCCACCACAGGACCCAGCTCATCTACAGGAGTGGCGGTGGGGACCTGCACA 3354
QY 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGGCTGGAGCCCTCTGAGAGGGAGGCCCCAGGTCTCCATGGCACCTCCGAAGGG 3414
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaLysGlyLeuGlnSer 764
Db 3415 GCTGGCTCCGATGATTTGATGTGACCTGGGAATGGGGCAGCAAGGGGCTGCAAGC 3474
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3535 CCCTCTGAGACTGATGGCTAGCTTGCCTGACCTGCAGCCCCCAGCCTGAATATGTG 3594
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3595 AACCAAGCCAGATGTTCCGGCCCCCAGCCCCCTTCGCCCCGAGAGGGCCCTCTGCCTGTGCC 3654
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLeuThrLeuSerProGlyLysAsnGlyVal 844
Db 3655 CGACCTGCTGGTGGCACTCTGGAAAGGCCCAAGACTCTCTCCCAAGGAAGATGGGGTC 3714
QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3715 GTCAAAAGACGTTTTTGGCTTTGGGGGTGCGGTGGAGAACCCCGAGTACTTGCACACCCAG 3774
QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGCTGCCCTCAGCCCCCAGCTCTCTCTGGCTTCAGCCAGCCTTCGACAACTC 3834
QY 885 TyrTyrTrpAspGlnAspProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGACCAAGACCCACCAAGCGGGGGGCTCCACCCAGACCTTCAAGAGGACCA 3894
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTAGCGAGAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3939
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RESULT 8

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US-10-101-510-81
; Sequence 81, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-81
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Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 15 Gaps: 1
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US-09-493-480-6 (1-919) x US-10-101-510-81 (1-4473)

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Db 175 ATGGAGCTGGCGCTTGTGCGCTGGGGCTCTCTCGCCCTCTTGGCCCCCGAGCC 234
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCGAGACCCCAAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCCTGCAGTCCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 295 ACCCAGCTGGACATGCTCCGCCACCTCTTACCAGGGGTGCCAGGTGGTGCAGGGAAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
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355 GAACCTACCTACCTGCCACCAATGCAGCGTCTCTCTCCAGGATATCCAGGAGTG 414
QY
81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
Db
415 CAGGGCTACGTCTCATCGCTCACACCAAGTGAGCGAGTCCCATGTCAGAGGCTGCGG 474
QY
101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db
475 ATTGTCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTACAAATGGA 534
QY
121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db
535 GACCCGCTGAACATACCAACCCCTGTGCACAGGGCCCTCCCCAGGAGGCTCGGGAGCTG 594
QY
141 GlnLeuArgSerLeuThrGlnIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db
595 CAGCTTCGAAGCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCCCAG 654
QY
161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
Db
655 CTCGTCTACGAGACACGATTTTGTGAAGAGACATCTTCCAAAGAACCAACAGCTGGCT 714
QY
181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db
715 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGAAG 774
QY
201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db
775 GGCTCCCGCTGTGGGAGAGAGATTCTGAGGATTTGTACAGAGCTGACGCGCACTGTCTGT 834
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221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db
835 GCCGTGGCTGTGCCCGCTGCAGAGGGCCACTGCCCACTGACTGTGCCATGAGCAGTGT 894
QY
241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db
895 GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGCGCTGGCTGCCCTCACCTTCAACCA 954
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261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db
955 AGTGCACTGTGTAGCTGCACTGCCAGCCCTGGTCACTACCAACACAGACACGTTTGAG 1014
QY
281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db
1015 TCATGCCCAATCCCGAGGGCCGGTATACATTCGGGCCAGCTGTGTGACTGCTGCTGCC 1074
QY
301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db
1075 TACAACTACTTTCTACGGACGTGGATCCTGCACCCCTCGTCTGCCCTGCACAAACCAA 1134
QY
321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db
1135 GAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAAGTGCAGCAAGCCCTGTGCCCGA 1194
QY
341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db
1195 GTGTGCTATGGTCTGGGCATGAGCACTTGCAGAGGTGAGGCGAGTTACCAAGTCCCAAT 1254
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361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db
1255 ATCCAGGAGTTTGTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAG 1314
QY
381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
Db
1315 TTTGATGGGGACCCAGCCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1374
QY
401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
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1375 GAGACTCTGGAGAGATCACAGGTTACCTATACATCTGAGCATGGCCGAGCAGCTGCCT 1434
QY
421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
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Db
1435 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGAGCAATTTCTGCACAATGGCGCC 1494
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441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
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1495 TACTCGCTGACCTCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCCTCACTCAGGGAA 1554
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461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
Db
1555 CTGGGACGTGGACTGGCCCTCATCCACCATAACCCACCTCTGCTTCTGTCGACAGGTG 1614
QY
481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db
1615 CCCTGGGACAGCTCTTTCGAAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1674
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501 GluAspGluCysValGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db
1675 GAGGACGAGTGTGTGGGAGGGCTGGCTGCCACCAGCTGTGGCCCGAGGGCACTGC 1734
QY
521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db
1735 TGGGCTCCAGGGCCACCCAGTGTCTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC 1794
QY
541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db
1795 GTGAGGAGTAATCCGAGTACTGCAGGGGTCTCCAGGAGTATGTGAATGCCAGGCACTGT 1854
QY
561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db
1855 TTGCCGTGCCACCTTGAGTGTGAGCCCAAGAAATGCTCAGTGACCTGTTTTGGACGGAG 1914
QY
581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
Db
1915 GCTGACCACTGTGTGGCTGTGCCCTGTGCCACTATAGGACCCTCCCTTCTGCGTGGCCGCTGC 1974
QY
601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
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621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db
2035 GCGCATGCCAGCTTGCCCCATCAACTGACCCACTCTCTGTGTGACCTGTGATGACAAG 2094
QY
641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db
2095 GSGTCCCCCGCGACAGAGAGCCAGCCCTCTGACGTCCATCATCTCTCGCGTGTGGC 2154
QY
653 2155
Db
2155 ATTTCTGCTGTCGTGTCCTTGGGGGTGGTCTTTTGGGATCTCTCAAGCGACGGCAGCAG 2214
QY
653 2215
Db
2215 AAGATCCGGAAGTACACGATGGGAGACTGTCTGAGGAAACGGAGCTGTGTGGAGCGCGCTG 2274
QY
653 2275
Db
2275 ACACCTAGCGGAGCGATGCCCAACCGAGCGCAGATGCCGATCCTGAAAGAGAGCGAGCTG 2334
QY
653 2335
Db
2335 AGGAAGGTGAAGTGTGATCTGGCGCTTTTGGCAGACAGTCTACAAGGGCATCTGGATC 2394
QY
653 2395
Db
2395 CCTGATGGGAGAAATGTGAAAATTCAGTGGCCATCAAAAGTGTGTGGGAAACACATCC 2454
QY
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2455 CCAAAGCAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGGGCTCCCCA 2514
QY
653 2515
Db
2515 TATGTCTCCCGCTTCTGGGCATCTGCTGTGACATCCACGGTGCAGCTGTGTGACACAGCTT 2574

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QY 653 ----- 653
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Db 2635 GACCTGTGAACGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2694
QY 653 ----- 653
Db 2695 CTCGTACACAGGACTTGGCGCTCGGAACGTGTGTCAAGAGTCCCAACCATGTCAAA 2754
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Db 2755 ATTACAGACTTCGGGCTGGCTCGGCTGTGGACATTGACGAGACAGAGTACCATGCAGAT 2814
QY 653 ----- 653
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QY 653 ----- 653
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QY 653 ----- 653
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QY 653 ----- 653
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QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGGACCCCGCGCTTTGTGGTCATCCAGAATGAGGACTTGGGCCCGAGCAGTCCCTTG 3174
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGACCTTCTACCGCTCACGTGCTGAGGAGCATGACATGGGGGACCTGGTGGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTACCCAGCAGGGCTTCTTCTGTCCAGACCTTGGCCCGGGCGCTGGG 3294
QY 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3295 GGCATGGTCCACACAGGCACCGCAGCTCATCTACCAGGAGTGGCGTGGGACCTTGACA 3354
QY 725 LeuGlyLeuGluProSerGluGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3355 CTAGGGCTGGAGCCCTCTGAAGAGGAGGGCCCGCCAGAGTCTCCACTGGCACCTCCGAAGG 3414
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyLeuGlnSer 764
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QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
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QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
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QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
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QY 865 GlyGlyAlaAlaProGlnProHisProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3775 GGAGGAGCTGCCCTCAGCCCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3834
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3835 TATTACTGGGACGAGGACCCAGAGCGGGGGCTCCACCCAGCACCTTTCAAAGGGACA 3894
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3895 CCTACGGCAGAGAACCCAGAGTACCTGGGTCTGGACGTGCCAGTG 3939
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RESULT 9

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US-10-762-128-5
; Sequence 5, Application US/10762128
; Publication No. US20040219161A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409C1
; CURRENT APPLICATION NUMBER: US/10/762,128
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 09/441,411
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-762-128-5
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Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 4900.00 Matches: 919
Percent Similarity: 73.23% Conservative: 0
Best Local Similarity: 73.23% Mismatches: 0
Query Match: 96.49% Indels: 336
DB: 20 Gaps: 1
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US-09-493-480-6 (1-919) x US-10-762-128-5 (1-4473)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 235 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGGGGCTCTCTCTCTCTCTCTCTCT 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnAsnLeu 60
Db 295 ACCACCTCGACATGTCTCGCCACCTCTACCGAGGCTGGCAGGTGGTGGCAGGAAACCTG 354
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 355 GAACTCACCTACCTGCCCCCAATGCGAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 414
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 415 CAGGGCTACGTGCTCATCTGCTCAACCAAGTGAAGCAGGTCCCACTTGCAGAGGCTTGGCG 474
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QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
DB 535 GACCCGCTGAACAATACCAACCCCTGTTCACAGGGGCTCCCCAGGAGGCGTGGGAGCTG 594
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 595 CAGCTTCGAAGGCTCACAGAGATCTTTGAAGAGGGGTCTTATCCAGGGAAACCCCGAG 654
QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
DB 655 CTCCTGCTACGAGACACAGATTTTGTGAAGGACATCTTCCACAAGAACAACAGCTGGCT 714
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 715 CTCACACTGATAGACCAACCGCTCTCGGGGCTGCGACCCCTGTTCTCCGATGTGAAG 774
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 775 GGCTCCCGCTGCTGGGAGAGATTCTGAGGATTGTGAGAGCTGACGGCCTGCTGCTGT 834
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
DB 835 GCCGTGGCTGTGCCGCTGCAAGGGGCCACTGCCACTGACTGCTGCCATGAGCAGTGT 894
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 895 GCTGCGGCTGACCGGGCCCAAGCACCTGACTGCTGCTGGCTGCTCCACTTCAACCAC 954
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 955 AGTGGCATCTGTAGCTGTCACCTGCCAGCCCTGGTCACCTACACACAGACAGCTTTGAG 1014
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 1075 TACAACCTACTCTTACGGACGTGGGATCTGCACCCCTGCTGCGCCCTGCACAAACCAA 1134
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 1135 GAGGTGACAGCAGAGATGCAACACACGCGGTGTGAGAAGTGCAGCAGCCCTGTGCCCGA 1194
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1195 GTGTGCTATGGTCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACCAGTGCCTAAT 1254
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1255 ATCCAGGAGTGTGCTGGCTGCAAGAAGATCTTTGGGAGCGTGGCATTTCTCGCGGAGAGC 1314
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGlnLeuGlnValPhe 400
DB 1315 TTTGATGGGAGCCCGACCTTCCAACACTGCCCGCTCCAGCCAGCAGCAGCTCCAAGTGT 1374
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
DB 1375 GAGACTCTGGAAGAGATCACAGGTTTACCTATATACATCTCAGCATGGCCGAGCAGCTGCCT 1434
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1435 GACCTCAGCGCTCTTCCAGAACCTTGAAGTAATCCGGGGACGAATTTCTGCACAATGGCGCC 1494
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1495 TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTCAGTAGGGAA 1554
QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuLeuCysPheValHisThrVal 480

DB 1555 CTGGCAGTGGACTGGCCCTCATCCACCATAACACCACCTCTGCTTCGTGCACACGGTG 1614
QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1615 CCCTGGGACCAAGCTCTTTCGGAAACCCGACCCAGGCTGTGCTCCACACTGCCAACCGGCCA 1674
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1675 GAGGACGAGTGTGTGGCGAGGGCCCTGGCCTGCCACACAGCTGTGCGCCGAGGGCACTGC 1734
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1735 TGGGCTCCAGGCGCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC 1794
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1795 GTGGAGGAATCCGAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1854
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1855 TTGCGCTGCCACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1914
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
DB 1915 GCTGACCAAGTGTGGCCTGTGCCCACTATAAGGACCCCTCTCTGCTGGCGCCGCTGC 1974
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
DB 1975 CCCAGCGTGTGAACCTGAGCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 2034
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
DB 2035 GCGCATGCCAGCTTGCCCATCACTCACTCACTCTCTGTGTGGACCTGATGACAAAG 2094
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
DB 2095 GGTCTCCCGCGCAGCAGAGAGCCAGCTCTGTGAGCTCCATCATCTCTGCGTGGTGGC 2154
QY 653 ----- 653
DB 2155 ATCTGCTGTCGTGGTCTTGGGGGTGGTCTTTGGGATGCTCATCAGCGACGGCAGCAG 2214
QY 653 ----- 653
DB 2215 AAGATCCGGAAGTACACGATGCGGAGACTGTCTGCAGGAAACGAGCTGTGTGGACCGCTG 2274
QY 653 ----- 653
DB 2275 ACACCTAGCGGAGCGATGCCCAACCGCGCAGATGCCGATCCTGAAAGAGACGGAGCTG 2334
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DB 2335 AGGAAGGTGAAGTGTGGATCTGGCGCTTTTGGCACAGTCTACNAGGGCATCTGGATC 2394
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DB 2395 CCTGATGGGAGAAATGTGAATAATCCAGTGGCCATCAAAGTGTGTAGGGGAAACACATCC 2454
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DB 2455 CCCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGTGTGGCTCCCCA 2514
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QY 653 ----- 653
DB 2575 ATGCCCTATGGCTCTCTTAGACCATGTCCGGGAAACCGCGGAGCCTGGCTGCCAG 2634
QY 653 ----- 653

Db	2635	GACCTGCTGAAC	CTGGTGTATGC	ATTGCCAAAGGGATG	AGCTACCTCGGAGGATG	TCGGG	2694
Qy	653	-----	-----	-----	-----	-----	653
Db	2695	CTCGTACACAGG	ACTTGGCCGCTCG	GNACGTGCTG	TGTCAGAGTCC	CAACCATGTCAA	2754
Qy	653	-----	-----	-----	-----	-----	653
Db	2755	ATTACAGACTT	CGGCGTCTGCG	TCTGCGCAT	TTCACGACAG	AGATACCATG	2814
Qy	653	-----	-----	-----	-----	-----	653
Db	2815	GGGGCAAGT	GCCCATCAAG	TGGATGGCG	TGAGTCCAT	TTCGCCCGCGGT	2874
Qy	653	-----	-----	-----	-----	-----	653
Db	2875	CACCAGAGT	GATGTGTGG	AGTTATGGT	TGACTGTGG	AGCTGATGACT	2934
Qy	653	-----	-----	-----	-----	-----	653
Db	2935	AAACCTTAC	GATGGATCCC	AGCCCGGAG	ATCCCTGAC	TCTGGA	2994
Qy	653	-----	-----	-----	-----	-----	653
Db	2995	CTGCCCAAG	CCCCCATCTG	CCACCAT	TGATGCTAC	ATGATCAT	3054
Qy	653	-----	-----	-----	-----	-----	653
Db	3055	ATTGACTCT	GAAATGTGG	CCCAAGATT	CGGGAGTTG	TGTCGA	3114
Qy	654	-----	-----	-----	-----	-----	654
Db	3115	AGGACCCCC	AGCGCTTGT	TGGTCAT	CCAGAA	TGAGGACT	3174
Qy	665	ASPserThr	PheTyrArg	SerSerLeu	LeuLeuAsp	AspMetGly	684
Db	3175	GACAGCAC	CTTCTACCG	TCTACTCTG	AGGACCAT	GACATGGG	3234
Qy	685	GluGluTyr	LeuValPro	GlnGlnGly	PhePheCys	ProAspPro	704
Db	3235	GAGGAGTAT	CTGGTACCC	ACAGGGCT	CTTCTTGT	CCAGACC	3294
Qy	705	GlyMetVal	HisHisArg	HisArgSer	SerSerThr	ArgSerGly	724
Db	3295	GGCATGGT	CCACACAC	AGCACCG	CAGCTCAT	TACAGGAG	3354
Qy	725	LeuGlyLeu	GluProSer	GluGluGlu	AlaProArg	SerProLeu	744
Db	3355	CTAGGGT	TGGAGCCCT	CTGAAGAG	AGAGGCC	CCCCAGG	3414
Qy	745	AlaGlySer	AspValPhe	AspGlyAsp	LeuGlyMet	GlyAlaAla	764
Db	3415	GCTGGCT	CCGATGAT	TATTTGAT	TGGTGACT	TGGGAAT	3474
Qy	765	LeuProThr	HisAspPro	SerProLeu	GlnArgTyr	SerGluAsp	784
Db	3475	CTCCCCA	CACATGAC	CCCCAG	CCCTCTAC	AGGGTAC	3534
Qy	785	ProSerGlu	ThrAspGly	TyrValAla	ProLeuThr	CysSerPro	804
Db	3535	CCCTCTG	AGATGATG	GTACGTTG	CCCCCTG	ACCTGC	3594
Qy	805	AsnGlnPro	AspValArg	ProGlnPro	ProSerPro	ArgGluGly	824
Db	3595	AACCAGC	CAGATGTT	TCGGCCCC	ACGCCCTT	TCGCCCG	3654
Qy	825	ArgProAla	GlyAlaThr	LeuGluArg	ProLysThr	LeuSerPro	844
Db	3655	CGACTGCT	GGTGCC	ATCTCTG	GAAGGCC	CAAGACT	3714
Qy	845	ValLysAsp	ValPheAla	PheGlyGly	AlaValGlu	AsnProGlu	864
Db	3715	GTCAAA	GACGTTTT	TGCTTTG	GGGGTGG	CGGTGG	3774

Qy	865	GlycylalalalProGlnProHisProAlaPheSerProAlaPheAsnLeu	884
Db	3775	GGAGGAGCTGCCCTCAGCCACCACCTCTCTCTGCGCTTCAGCCAGCCTTCGACAACCTC	3834
Qy	885	TyTyTrpAspGlnAspProProGluuAagGlyAlaProProSerThrPheIysGlyThr	904
Db	3835	TATTACTGGGAGCAGGAGCCACCAGAGCGGGGGGCTCCACCCAGCACCTTTCAAAGGGACA	3894
Qy	905	ProThrAlaGluAsnProGluTyuLeuGlyuLeuAspValProVal	919
Db	3995	CCTACGCGCAGAGAACCCAGAGTAGTACCTGGGTCTCGACGTGCCAGTGTG	3939
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; Sequence 8, Application US/10723860			
; Publication No. US20040253606A1			
; GENERAL INFORMATION:			
; APPLICANT: Aziz, Natasha			
; APPLICANT: Ginsburg, Wendy M.			
; APPLICANT: Zlotnik, Albert			
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &			
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators			
; FILE REFERENCE: 05882, 0193.NPUS01			
; CURRENT APPLICATION NUMBER: US/10/723,860			
; CURRENT FILING DATE: 2003-11-26			
; PRIOR APPLICATION NUMBER: 60/429,739			
; PRIOR FILING DATE: 2002-11-26			
; NUMBER OF SEQ ID NOS: 8393			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 8			
; LENGTH: 4473			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-723-860-8			

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Db	595	CAGCTTCGAAGCCTCAGAGATCTTGAAGAGGGGCTCTTGATCCAGCGGAACCCCCAG	654	Db	1675	GAGGACGAGTGTGGCGAGGGCTTGGCTGCCACAGCTGTGCCCGGAGGGCACTGC	1734
QY	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180	QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	655	CTCTGCTACCAGGACAGATTTTGTGGAAGGACATCTCCACAAGAAACAACAGCTGGCT	714	Db	1735	TGGGGTCCAGGGCCCAACCAGTGTCTCAACTGCAGCAGTTCCTTCGGGGCCAGGAGTGC	1794
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200	QY	541	ValGluGluCysArgValLeuGlnGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
Db	715	CTCACACTGATAGACCAACACGCTCTCGGGCCCTGCCACCCCTGTTCTCCGATGTGTAAG	774	Db	1795	GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCAAGGAGATATGTGAATCCCAAGGCACTGT	1854
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220	QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
Db	775	GGCTCCCGCTGTGGGAGAGAGATTCTGAGGATTGTGAGAGCTGACGGCCTGACGGCAGTGT	834	Db	1855	TTGCCGTGCCACCTTGAGTGTGAGCCCCAGANTGGCTCAGTGACCTGTTTTGGACCGGAG	1914
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240	QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
Db	835	GCCGCTGGCTGTGCCGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT	894	Db	1915	GCTGACCAGTGTGGCCTGTGCCACTATAAGGACCCCTCCCTCTGCGTGGCCGCTGC	1974
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260	QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
Db	895	GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGCTGCGCTGCCCTCCACTTCAACCAC	954	Db	1975	CCCAAGCGGTGAAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	2034
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
Db	955	AGTGGCATCTGTGAGCTGCACGCCCGCCCTGGTCACCTACAACACAGACAGCTTTGAG	1014	Db	2035	GGCGCATGCCAGCTTGCCCCATCACTGCACCCCACTCTCTGTGTGGACCTGGATGACAAG	2094
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300	QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	1015	TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGGCCAGCTGTGTGCTGCC	1074	Db	2095	GGCTGCCCGCCGAGCAGAGAGCAGCCCTCTGAGCTCCATCATCTCTCGGTGGTTGGC	2154
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	QY	653	-----	653
Db	1075	TACAACCTACTCTTACTACGACGTGGGATCTCTGCACCCCTGCTGCCCCCTGCACAACCAA	1134	Db	2155	ATTCTGCTGTCGTGGTCTTTGGGGTGGTCTTTTGGGATCCTCATCAAGCGACGGCAGCAG	2214
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	QY	653	-----	653
Db	1135	GAGGTGACAGCAGAGATGGACACACAGCGGTGTGAGAACTGCAGCAGCCCTGTGCCCGA	1194	Db	2215	AAGATCCGGAAGTACACGATGCGGAGACTGTCTGCAGGAAACGGAGCTGGTGGAGCCGCTG	2274
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	QY	653	-----	653
Db	1195	GTGTGCTATGGTCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACCAAGTGCCAAT	1254	Db	2275	ACACCTAGCGGAGCGATGCCCAACGAGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG	2334
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	QY	653	-----	653
Db	1255	ATCCAGGAGTTTGTGGCTGCAAGAAAGATCTTTGGGAGCCTGGCATTTCTGCGGAGAGC	1314	Db	2335	AGGAAGGTGAAGTGTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC	2394
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGlnLeuValPhe	400	QY	653	-----	653
Db	1315	TTTGATGGGGACCCAGCCTTCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1374	Db	2395	CCTGATGGGAGAATGTGAAAATTCCAGTGGCCATCAAAGTGTGAGGGAAAAACACATCC	2454
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	QY	653	-----	653
Db	1375	GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGACAGCCTGCCT	1434	Db	2455	CCCAAAGCCAAACAAGAAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	2514
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	QY	653	-----	653
Db	1435	GACCTCAGCGTCTTCAGAACCTGCAAGTAATCCGGGGAGCGAATTCGACCAATGGCGCC	1494	Db	2515	TAATGCTCCCGCTTCTGGGCAATCTGCCCTGACATCCACGGTGCAGCTGGTGTGACACAGCTT	2574
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460	QY	653	-----	653
Db	1495	TACTCGCTGACCTTGCAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTCAGTGGGAA	1554	Db	2575	ATGCCCTATGGCTGCTCTTAGACCATCTCCGGGAAAACCGCGGACGCTGGGCTCCCAG	2634
QY	461	LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal	480	QY	653	-----	653
Db	1555	CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACTCTCTGCTTCGTGCACACGGTG	1614	Db	2635	GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCG	2694
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	QY	653	-----	653
Db	1615	CCCTGGGACAGCTCTTTTGGAAACCCGCAACGCTCTCTCCACTGCCAACCGGCCA	1674	Db	2695	CTCGTACACAGGGACTTGGCCGCTCGGAACGTGTGGTCAAGAGTCCCCAACCATGTCAAA	2754
				QY	653	-----	653


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Qy 653 -----
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Qy 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGACCCCCAGCGCTTTGTGGTCATCCGAATGAGGACTTGGGCCCGCAGTCCTCGTTG 3174
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Db 3235 GAGGAGTATCTGTGTACCCAGCAGGGCTTCTGTCTCAGACCTGCCCCGGCGCTGGG 3294
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3295 GGCATGTGTCCACACAGCAGCCGAGCTCATCTACCGAGAGTGGCGGTGGGACCTGTACA 3354
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; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; FILE REFERENCE: 30448 103-US-UI
; CURRENT APPLICATION NUMBER: US/10/207,498
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
; US-10-207-498-5

Alignment Scores:
Pred. No.: 0 Length: 3765
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 15 Gaps: 1

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Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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Db 3061 GAGAGTATCTGGTACCCAGAGGGCTTCTTCTCCAGACCTTGGCCCCGGCGCTGGG 3120
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCATGCTCCACCACAGCCAGCTCATCTACCCAGGAGTGGCGTGGGGACCTTGACA 3180
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCGCCAGGTCTCCACTGGCACCTCCGAGGG 3240
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGTGACCTGGGAATGGGGCAGCCCAAGGGGCTGCAAGC 3300
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCCCACATGACCCCGCCCTCTACAGCGGTACAGTGAGGACCCCAAGTACCCCTG 3360
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCCTCTGAGACTGATGGCTACGTTGCCCTGACCTGACGCCGCCAGCCCTGAATATGTG 3420
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACGAGCAGATGTTGGCCCCAGCCCCCTTCGCCCGAGGGCCCTCTGCCCTGTGCC 3480
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGGTCCACTCTGGAAAGGGCCCAAGACTCTCTCCCGAGGAAGATGGGGTC 3540
QY 845 ValLysAspValPheAlaPheGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAAAGACCTTTTGGCTTTGGGGTGGCGTGGAGAACCCCGAGTACTTTGACACCCAG 3600
QY 865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCCCTCAGCCCCACCTTCTCTGCTTTCAGCCAGCTTTCGACCAACCTC 3660
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACGAGGACCCACAGAGCGGGGGCTCCACCCAGACCTTCAAGGGACA 3720
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919

Db 3721 CCTACGCGAGAAACCAGAGTACTGGGTCTGGACGTGCCAGTG 3765
RESULT 12
US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; TITLE OF INVENTION: ANTI-BODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT. 073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-123-8
Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
Gaps: 1
US-09-493-480-6 (1-919) x US-09-811-123-8 (1-3768)
QY 1 MetGluLeuAlaAlaLeuCysArgTyrGlyLeuLeuAlaLeuProGlyAla 20
Db 1 ATGAGCTGGCGCCTTGTGCGCTGGGGCTCTCTCTCGCCCTCTTGGCCCCGGAGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCACCAAGTGTGCACCGGCACAGACATGAAGCTGGCGCTCCCTGCCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGGACATGTCTCGCCACCTCTACCGGGCTGCCAGGGTGGTGCAGGGAAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACTCACCTACTGCGCCACCAATGCCAGCTGTCTCTCTCGCAGGATATCCAGGAGGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGTCTATCGCTCACACCAAGTGAAGTGGCAGGTCCCACTGCAGAGGCTCGCG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGCCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGACAAATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACATATACCACTGTCACAGGGGCCCTCCCGAGAGGCTTGGGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCCTCACAGAGATCTTTGAAAGGAGGGGTCTTGTATCCAGCGGAAACCCCGAG 480
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACGAGACACGATTTTGTGGAAGGACATCTTCCACAAAGAACCAACAGCTGGCT 540

Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
Db	541	CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAAG	600
Qy	201	GlySerArgCysTrpGlyGlySerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	601	GGGTCCCGCTGCTGGGGAGAGAGTTCTGAGGATTGTTCAGAGCCTGCACGCGCACTGTCTGT	660
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
Db	661	GC CGGTGGCTGTGCCCCCTGCAAGGGGCCACTGCCCACTGACTGCTGCCAATGAGCAGTGT	720
Qy	241	AlaAlaGlyCysThrGlyProCysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	721	GCTGCCGGCTGCACGGSCCCCAAGCACTCTGACTGCTGCCCTGCCCTCCACTTCAACCCAC	780
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
Db	781	AGTGGCATCTGTGAGCTGTCATGCCCCAGCCCTGGTCACTTACCAACACAGACACAGTTTGAG	840
Qy	281	SerMetProAsnProGluGlyArgTyrThrPheGlyValaSerCysValThrAlaCysPro	300
Db	841	TCCATGCCCAATCCGAGGGCCGGTATACATTTGGCGCCAGCTGTGTGACTGCTGTGCC	900
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	901	TACAACTACCTTCTACGGACGTGGGATCTGCACCCCTGCTGCCCTCCGACACACCA	960
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluIysCysSerIysProCysAlaArg	340
Db	961	GAGGTGACAGCAGAGGATGGAACACACACGGGTGTGAGAAGTGCAGCAAGCCTGTGCCCGA	1020
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
Db	1021	GTGTGCTATGCTGTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACGATGGCCAAT	1080
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1081	ATCCAGAGATTGCTGGCTGCAGAGAATCTTTGGAGCCTGGCAATTTCTGCCGAGAGC	1140
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
Db	1141	TTTGTATGGGACCACAGCCTCCAACTGCCCGCTCCAGCCAGACGAGCTCCAAGTGT	1200
Qy	401	GluThrLeuGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
Db	1201	GAGACTCTGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGAGACGCTGCCT	1260
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyVala	440
Db	1261	GACCTCAGCGTCTCCAGAACCTTGCAGTAAATCCGGGGAGCAATTTGTCACATGGGCC	1320
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
Db	1321	TACTCGTGACCTGCAAGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGGAA	1380
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
Db	1381	CTGGGCAGTGGACTGGCCCTCATCCACCAATAACCCACCTCTGCTGTGTGCAACGGTG	1440
Qy	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
Db	1441	CCCTGGAGACAGCTCTTTTCGGAACCCCGACCAAGTCTGTCTCCACATGTCACACCGGCCA	1500
Qy	501	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
Db	1501	GAGSACGAGTGTGTGGCGAGGGGCTGGCCTGCCACCACTGTGTGGCCCGAGGGCACTGC	1560
Qy	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	1561	TGGGGTCCAGGGGCCACCAAGTGTGTCACTGCAGCCAGTTCCTTCTGGGGCCAGGAGTGC	1620

QY	541	ValGluGlnCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
DB	1621	GTGAGGAATGCCAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGCACTGT	1680
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	1681	TTGCCGTGCCACCCTGAGTGTCAAGCCCCAGAAATGGCTCAGTGACCTGTTTGGACCCGGAG	1740
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
DB	1741	GCTGACCAGTGTGTGGCTGTGCCCATATAAGAACCTCCCTCTTCGCTGGCCCGCTGC	1800
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
DB	1801	CCCAGCGTGTGAACCTGACCTCTCTCATGCCCATCTGGAAGTTCCAGATGAGGAG	1860
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640
DB	1861	GGCGCATGTCAGACCTTGGCCCATCAATGCGACCACTCCTGTGTGGACCTGGATGACAAG	1920
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
DB	1921	GGCTGCCCCCGAGCAGCAGAGACGCCCTCTGACCTCCATCGTCTCTGGGTGGTTGSC	1980
QY	653	-----	653
DB	1981	ATTCTGCTGTCGTGTGCTTTGGGGTGGTCTTTGGGATCTCTCATCAAGCGACGGCAGCAG	2040
QY	653	-----	653
DB	2041	AAGATCCGGAAGTACAGATGCGGAGACTGCTCAGGAAACGGAGCTGTTGGAGCCGCTG	2100
QY	653	-----	653
DB	2101	ACACCTAGCGGAGGATGCCAACACAGGCGCAGATCGGGATCTCTGAAAGAGACGGAGCTG	2160
QY	653	-----	653
DB	2161	AGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC	2220
QY	653	-----	653
DB	2221	CCTGATGGGAGAAATGTGAAAATTCAGTGGCCATCAAAGTGTGTGAGGGAAAAACATCC	2280
QY	653	-----	653
DB	2281	CCCAAGCCCAAGAAATCTTAGAAGAAAGCATAGTGATGGCTGTTGGCTCCCCCA	2340
QY	653	-----	653
DB	2341	TATGTCTCCGCTTCTGGGCATCTGCTGACATCCACGTCAGCTGTTGTGACACAGCTT	2400
QY	653	-----	653
DB	2401	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAAACCGCGAGCCCTGGGCTCCAG	2460
QY	653	-----	653
DB	2461	GACCTGTGAACCTGGTGTATGCAGATTGCCAAGGGATGAGCTACTGGAGGATGTGCGG	2520
QY	653	-----	653
DB	2521	CTCGTACACAGGAGCTTGGCCGCTCGGAAGTCTGTTCAAGAGTCCCAACCATGTCAAA	2580
QY	653	-----	653
DB	2581	ATTACAGACTTCGGGCTGGCTCGGCTGCTGGAATTCACGAGACAGAGTACCATGCAGAT	2640
QY	653	-----	653
DB	2641	GGGGCAAGTGGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTTACC	2700
QY	653	-----	653

Db 2701 CACCAGAGTATGTGGAGTTATGGTCACTGTGTGGAGGCTGATGACTTTTGGGGCC 2760
Qy 653 ----- 653
Db 2761 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTCTGGAAGAGGGAGCGG 2820
Qy 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGTGTCAAATGTTGGATG 2880
Qy 653 ----- 653
Db 2881 ATTGACTCTGAATGTGGCCCAAGATCCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC 2940
Qy 654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGAGCCCCAGCGCTTTGTGGTCAATCCAGAAATGAGGACTTGGGCCAGCCAGTCCCTTG 3000
Qy 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGACCTTCTACCGCTCACTGTGGAGGACGATGACATGGGGGACCTGTGTGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTATCCCCAGCAGGGCTTCTCTGTCAGACCTGCCCCGGGGCGCTGGG 3120
Qy 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGCATGGTCCACACAGGACCCGACGCTCATCTACAGGAGTGGCGGTGGGACCTTGACA 3180
Qy 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGCCGCCAGGTCTCCACTGGCACCTCCGAAGGG 3240
Qy 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGTGACCTGGGAATGGGGGAGCCCAAGGGGCTGCAAGC 3300
Qy 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCACACATGACCCAGCCCTCTACAGCGGTACAGTGAAGACCCACAGTACCCCTG 3360
Qy 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCCTCTGAGACTGATGCTACGTTGCCCCCTGACCTGACGCCGCCAGCCCTGAATATGTG 3420
Qy 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCCAGCAGATGTTGGGCCCCAGCCCTTCGCCCGGAGAGGGCCCTCTGCTGTGCTCC 3480
Qy 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGGTCCACTCTGGAAGAGGCCCAAGACTCTCTCCCGAGGAAGATGGGGTC 3540
Qy 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAGAGCGTTTTTGCCTTTGGGGTGGCGTGGAGAACCCCGAGTACTTGACACCCCG 3600
Qy 865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGCTGCCCTCAGGCCCAACCTCTCTCTCTGCTTTCAGCCAGCCTTCGACCAACCTC 3660
Qy 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACCAAGGACCCAGAGCGGGGGCTCCACCCAGCACCTTTCAAGAGGACA 3720
Qy 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAACCCAGAGTACCTGGGTCTGGAGCTGCCAGTG 3765

RESULT 13

US-09-811-115-2

; Sequence 2, Application US/09811115
; Patent No. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Erickson, Sharon
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-811-115-2

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 9 Gaps: 1

US-09-493-480-6 (1-919) x US-09-811-115-2 (1-3768)

Qy 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTGTCCGCTGGGGCTCTCTCTCGCCCTTTGCGCCCGGAGCC 60
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAAGTGTGCACCCGCCACAGATCAAGCTGCGGGTCTCCCTGCCAGTCCCAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCCAGCTGGACATGCTCCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGGAACCTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAATCACCCTACCTGCGCCCAATGCCAGCTCTCTCTCTCTGCGAGGATATCCAGAGGTG 240
Qy 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGCTCATCGCTCAACCAAGTGAAGGAGGTGCCACTGCAGAGGCTCGGG 300
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCGGTGTAGACAAATGA 360
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAAATACCACTCCCTGTACAGGGGCTCCCGCAGAGGCTCGGGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuLeuGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCTCAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGAACCCCGAG 480
Qy 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCTGCTACAGGACACGATTTTGTGGAAGGACATCTTCCCAAGAACCAACACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAG 600
Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCGCTGCTGGGGAGAGAGTTCTGAGGATTTGTGAGGCTGTGAGGCTGAGCGCTGCTGT 660

QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
DB 661 GCCGTGGCTGCGCGCTGCAAGGGCCACTGCCACTGCTGCTGCATGAGCAGTGT 720
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 721 GCTGCGGGCTGACGGGCCCAAGCACCTGACTGCTGCGCTGCTCCACTCAACCAAC 780
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 781 AGTGGCATCTGTAGCTGCACTGCCAGCCCTGGTCACTCAACACAGACACGTTTGAG 840
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 841 TCCATGCCAATCCCGAGGGCCGGTATACATTCGGGCCAGCTGTGTACTGCCCTGTGCC 900
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
DB 901 TACAACCTACCTTCTACGGACGTGGATCCTGCACCCCTCGTCTGCCCTGCACAAACAA 960
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
DB 961 GAGGTGACAGCAGAGATGGAAACACAGCGGTGTGAGAGTGAGCAAGCCCTGTGCCCGA 1020
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1021 GTGTGCTATGCTTGGGCATGAGCAGCTTGCAGAGGTGAGGGCAGTTACCACTGCCAAT 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1081 ATCCAGGAGTTTGTGGCTGCAAGAAGATCTTTGGGAGCTGGCATTTCTGCCGGAGAGC 1140
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1141 TTTGATGGGGACCCAGCCCTCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
DB 1201 GAGACTCTGGAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGACAGCTGCTCT 1260
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
DB 1261 GACCTCAGCGCTCTTCAGAACCTGCAAGTAATCCGGGAGCAATCTGCACAAATGGCGCC 1320
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
DB 1321 TACTGCTGACCTTCAAGGGCTGGGCATCAGCTGGCTGGGCTGGCTCACTGAGGGAA 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGCAGTGGACTGGCCCTCATCCACCAATACACCCACTCTGCTTCGTGCACAGGTG 1440
QY 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCTGGGACAGCTCTTTCCGAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCA 1500
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACGAGTGTGTGGGCCAGGGCTGGCTTGCACCACTGTCAGCTGGCGCCGAGGGCACTGC 1560
QY 521 TrrGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGGTCCAGGGCCACCCAGTGTGTCACTGCAGCCAGTTCTTTCGGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1621 GTGGAGGAATCCGAGTACTGCAGGGGCTCCCGAGGGAGTATGTGAATGCCAGGCACTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1681 TTGGCGTGCCACCTGAGTGTGAGCCCCAGAAATGGCTCAGTACCTGTATTGGACCGGAG 1740

QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
DB 1741 GCTGACCAGTGTGTGGCTGTGGCCACTATAAGGACCCTCCCTTCTGCGTGCCTGCG 1800
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrrLysPheProAspGluGlu 620
DB 1801 CCCAGCGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
DB 1861 GCGCATGCCAGCTTGGCCCATCACTGCACCCCACTCTCTGTGTGAGACCTGATGACAAG 1920
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer- 653
DB 1921 GGTGCCCCCGCGAGCAGAGAGCCAGCCCTCTGACGTCCATCGTCTCTGCGGTGGTTGCG 1980
QY 653 ----- 653
DB 1981 ATTCTGCTGGTGTGGTCTTGGGGGTGTCTTTGGGATCTCTCATCAGCGACGGCAGCAG 2040
QY 653 ----- 653
DB 2041 AAGATCCGGAAGTACACGATGCGGAGACTGTGTCAGGAAACGGAGCTGGTGAGCGCGTG 2100
QY 653 ----- 653
DB 2101 ACACCTAGCGGAGCGATGCCAACCGAGCGCAGATGCGGATCCTGAAAGAGACGGAGCTG 2160
QY 653 ----- 653
DB 2161 AGGAAGGTGAAGTGTCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220
QY 653 ----- 653
DB 2221 CCTGATGGGAGAATGTGAATAATCCAGTGGCCATCAAAAGTTTGAGGGAAACACATCC 2280
QY 653 ----- 653
DB 2281 CCCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGTGGTGTGGCTCCCCA 2340
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DB 2341 TATGTCTCCCGCTTCTGGGCATCTGCCGTGACATCCACGGTGCAGCTGGTGTGACACAGCTTT 2400
QY 653 ----- 653
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QY 653 ----- 653
DB 2461 GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGGATGAGCTACTCTGGAGGATGTGCGG 2520
QY 653 ----- 653
DB 2521 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGCTGTCAAGAGTCCCCAACCATGTCAAA 2580
QY 653 ----- 653
DB 2581 ATTACAGACTTCGGGCTGGCTGGCTGTGGACATTGACGACAGACAGATTCCATGCGAGAT 2640
QY 653 ----- 653
DB 2641 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGCTTCAAC 2700
QY 653 ----- 653
DB 2701 CACCAGAGTGTGTGGAGTTTATGTTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
QY 653 ----- 653
DB 2761 AAACCTTACGATGGGATCCACGCCCGGAGATCCCTGACCTGCTGGAAGGGGAGCGG 2820
QY 653 ----- 653

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Db 2821 CTGCCCCAGCCCCCATCTCGACCATTTGATGTCTACATGATCATGTCAAATGTTGATG 2880
QY 653 -----
Db 2881 ATTGACTCTGAATGTCGGCCCAAGATTCCGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGAGCCCCCAGCGCTTTGTGGTCTATCCAGAAATGAGGACTTGGGCCCGCAGCTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGACCTTCTACCGCTCCTGCTGGAGGAGATGACATGGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGTATCCCCAGAGGGCTTCTTGTCTCCAGACCTGCCCGCGGGCTGG 3120
QY 705 GlyMetValHisHisArgHisArgSerSerThrArgSerGlyGlyAspLeuThr 724
Db 3121 GGCATGGTCCACACAGGCCCGCAGCTCATCTACAGGAGTGGCGTGGGACCTGACA 3180
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGGAGCCCTCTGAAGAGGAGGGCCCCCAGGTCTCCACTGGCACCCTCCGAAGGG 3240
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaValGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGTTATTTGATGTGACCTGGGAATGGGGGACGCCAAGGGCTGCAAGC 3300
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
Db 3301 CTCCCCACACATGACCCCGCCCTCTACAGCGGTACAGTGAGGACGCCACAGTACCCCTG 3360
QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
Db 3361 CCCTCTGAGACTGATGGCTACGTGTGCCCTTGCCTGACCTGACAGCCCCCAGCCTGAATATGT 3420
QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
Db 3421 AACCAGCCAGATGTTGGCCCCAGCCCCCTTCGCCCGAGAGGGCCCTCTGCTGTGCTGCC 3480
QY 825 ArgProAlaGlyAlaThrLeuGluArgProLysThrLeuSerProGlyLysAsnGlyVal 844
Db 3481 CGACCTGCTGCTGCTCACTCTGGAAGGGGCCCAAGACTCTCTCCCGAGGAAGATGGGTC 3540
QY 845 ValLysAspValPheAlaPheGlyAlaValIleuAsnProGluTyrLeuThrProGln 864
Db 3541 GTCAAAGACGTTTTTGCCTTTGGGGGTGGCGTGGAGAACCCCGAGTACTTGACACCCCGAG 3600
QY 865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 884
Db 3601 GGAGGAGTGGCCCTCAGCCCCACCTCTCTCTGCTTCCAGCCAGCCCTTCGACACCTC 3660
QY 885 TyrTyrTrpAspGlnAspProProGluArgGlyAlaProProSerThrPheLysGlyThr 904
Db 3661 TATTACTGGGACGAGGACCCACAGAGCGGGGGCTCCACCCAGCACCTTCAAAGGACA 3720
QY 905 ProThrAlaGluAsnProGluTyrLeuGlyLeuAspValProVal 919
Db 3721 CCTACGGCAGAGAACCCAGAGTACTTGGGGTCTGGAGTGGCCAGTG 3765
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RESULT 14

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US-09-984-092-3
; Sequence 3, Application US/09984092
; Publication No. US20040037840A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS
; FILE REFERENCE: P1011PC00
; CURRENT APPLICATION NUMBER: US/09/984,092
; CURRENT FILING DATE: 2001-10-26
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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
US-09-984-092-3
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Alignment Scores:

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Pred. No.: 0 Length: 3768
Score: 4992.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 93.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 11 Gaps: 1
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US-09-493-480-6 (1-919) x US-09-984-092-3 (1-3768)

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QY 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyVala 20
Db 1 ATGGAGCTGGCGGCTTGTGGCGCTGGGGCTCTCTCGCCCTCTTGGCCCCGGAGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCGCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCCACTGGACATGTCTCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGGAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACCTACCTACTGCGCCCAATGCGAGCTGTCTTCTTGAGGATATCCAGGAGGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGTCTATCGCTCACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCCTGTGATAGCAATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyValAspSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACATACACACCCCTGTACAGGGGGCTTCCAGAGGCGCTGCCGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCTCTACAGAGATCTTGAAGAGGGGGTCTTGATCCAGCGGAACCCCGAG 480
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCCTGTACACAGACACGATTTGTGAAGAGACATCTCCACAAGAACCAACAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTTGCCACCCCTGTTCTCGATGTGTAA 600
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGTGGGGAGAGATCTGAGGATTTGTGAGGATTTGTGAGGATTTGTGAGGAT 660
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 661 GCGGTGGCTGTGCGCGCTGCAAGGGGGCCACTGCCCACTGACTGCTGCATGAGCAGTGT 720
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGGCTGCACGGGGCCCCAAGCACTCTGACTGCTGGCTGCTGCTTCAACCCAC 780
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QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	Db	1861	GGCGCATGCCAGCCTTGCCCATCAACTCACTCTCTGTGTGACCTGTGATGACAAG	1920
Db	781	AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGGTCACTACACACACACACAGCTTTGAG	840	QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300	Db	1921	GGTCCCCCGCGAGCAGAGACCCACTCTGACGTCCATCGTCTCTGCGGTGTTGGC	1980
Db	841	TCCATGCCCAATCCCGAGGCGCGGTATACATTCGGCGCCAGCTGTGTGACTGCCTGTGCC	900	QY	653		653
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	Db	1981	ATTCTGCTGGTCTGTGGTCTTGGGGGTGGTCTTGGGGATCCTCATCAAGCGACGGCAGCAG	2040
Db	901	TACAACTACTCTTCTACCGAGCTGGGATCCTGCACCCCTCGTCTGCCCTCGTCACAAACAA	960	QY	653		653
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	Db	2041	AAGATCCGGAAGTACACGATCGGAGACTGTCTGCAGGAAACGGAGCTGTGTGGAGCGCTG	2100
Db	961	GAGGTGCACAGCAGAGGATGGAACACACAGCGGTGTGAGAACTGCAGCAGCCCTGTGCCGA	1020	QY	653		653
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	Db	2101	ACACCTAGCGGAGCGATGCCCAACGAGCGCAGATGCCGATCCTGAAAGAGACGGAGCTG	2160
Db	1021	GTGTGCTATGGTCTGGGCATGGAGCACTTGCAGAGAGTGGGCGAGTTACCAAGTGCCTAT	1080	QY	653		653
QY	361	IleGlnGluPheAlaGlyCysIleValIlePheGlySerLeuAlaPheLeuProGluSer	380	Db	2161	AGGAAGGTGAAGTGTCTGGATCTGGCGCTTTTGGCACAGTCTACAGGGCATCTGGATC	2220
Db	1081	ATCCAGAGTGTCTGGCTGCAAGAAAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGC	1140	QY	653		653
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe	400	Db	2221	CCTGATGGGAGATGTGAAAATTCAGTGGCCATCAAAAGTGTGAGGAAAAACACATCC	2280
Db	1141	TTTGTATGGGAGCCAGCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1200	QY	653		653
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	Db	2281	CCCAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTATGGTGGTGGTGGCTCCCA	2340
Db	1201	GAGACTCTGGAAGAGATCAGAGTTACCTATATACATCTCAGCATGGCGGACAGCCTGCCT	1260	QY	653		653
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	Db	2341	TATGTCTCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGCAGCTGTGTGACACAGCTT	2400
Db	1261	GACCTCAGCGCTTCTCAGAACCTGCAAGTAATCCGGGAGCAATCTGCACAAATGGCGCC	1320	QY	653		653
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460	Db	2401	ATGCCCTATGGCTGCTCTTAGACCATCTGCGGAAACCGCGAGCGCTGGGCTCCCA	2460
Db	1321	TACTCGCTGACCTGCAAGGCTGGGCATCAGCTGGCTGGGCTGGCTCACTGAGGAA	1380	QY	653		653
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480	Db	2461	GACCTGCTGAACACTGGTGTATGCAGATGCCAAGGGATGAGCTACTCTGGAGGATGTGGG	2520
Db	1381	CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCACCTCTGCTTCGTGCACACGGTG	1440	QY	653		653
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	Db	2521	CTCGTACACAGGACTTGGCCGCTCGGAACGTGTGTCTCAAGAGTCCCACCATGTCAA	2580
Db	1441	CCTTGGACAGCTCTTTTGGAAACCCGACCAAGCTCTCTCCACTGCCAACCGGCCA	1500	QY	653		653
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuLeuCysAlaArgGlyHisCys	520	Db	2581	ATTACAGACTTTCGGGCTGGCTGGGACATTGACGACAGAGATACCATGCAGAT	2640
Db	1501	GAGGACGAGTGTGGGCGAGGGCCTGGCTGCCACCACTGTGGCCCGAGGGCACTGC	1560	QY	653		653
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	Db	2641	GGGGGCAAGGTGCCCATCAAGTGGATGGCGTGGAGTCCATTCTCCGCCGGCGGTTCA	2700
Db	1561	TGGGGTCCAGGGCCCAACCAAGTGTGTCAACTGCAGCCAGTTCTTCTGGGGCCAGGATGC	1620	QY	653		653
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	Db	2701	CACCAGAGTGTGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC	2760
Db	1621	GTGGAGGAATCCGGAGTACTGCAGGGGCTCCCGAGGAGATGTGAATGCCAGGCACTGT	1680	QY	653		653
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580	Db	2761	AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGCTGGMAAAGGGGAGCGG	2820
Db	1681	TTGGCGTGCCACCTGAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTGGACCGGAG	1740	QY	653		653
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600	Db	2821	CTGCCCAAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGGTCAAAATGTTGGATG	2880
Db	1741	GCTGACCACTGTGTGGCCTGTGCCACTATAAGGACCTCCCTTCTGCGTGGCCGCTGC	1800	QY	653		653
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620	Db	2881	ATTGACTCTGAATGTGCGCAAGATTCGCGGAGTGGTGTCTGAATTCCTCCCGCATGGCC	2940
Db	1801	CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTCGAAGTTTCCAGATGAGGAG	1860	QY	654	-----GlnAsnGluAspLeuGlyProAlaSerProLeu	664
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys	640				


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Db 2941 AGGACCCCGAGCGCTTTGGTTCATCCAGAAATGAGACTTGGCCCGCAGCTGCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCACTGCTGAGAGACATGACATGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGGTACCCCGAGCGGCTTCTTGTCAGACCTGCCCCGGCGCTGGG 3120
QY 705 GlyMetValHisArgHisArgSerSerThrArgSerGlyGlyGlyAspLeuThr 724
Db 3121 GGATGGTCCACACAGCACCGCAGCTCATCTACAGGAGTGGCGGTGGGACCTTGACA 3180
QY 725 LeuGlyLeuGluProSerGluGluAlaProArgSerProLeuAlaProSerGluGly 744
Db 3181 CTAGGGCTGAGCCCTCTGAAGAGGAGGCCCGCCAGGTCTCCACTGGCACCTCCGAAGGG 3240
QY 745 AlaGlySerAspValPheAspGlyAspLeuGlyMetGlyAlaAlaGlyGlyLeuGlnSer 764
Db 3241 GCTGGCTCCGATGATTTGATGGTGAACCTGGGAATGGGGCAGCCAAAGGGCTGCAAGC 3300
QY 765 LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspProThrValProLeu 784
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QY 785 ProSerGluThrAspGlyTyrValAlaProLeuThrCysSerProGlnProGluTyrVal 804
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QY 805 AsnGlnProAspValArgProGlnProProSerProArgGluGlyProLeuProAlaAla 824
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QY 845 ValLysAspValPheAlaPheGlyGlyAlaValGluAsnProGluTyrLeuThrProGln 864
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QY 865 GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAlaPheAspAsnLeu 884
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RESULT 15

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US-10-280-576-3
; Sequence 3, Application US/10280576
; Publication No. US2004004405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280, 576
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-280-576-3
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Alignment Scores:

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Pred. No.: 0 Length: 3768
Score: 4892.00 Matches: 918
Percent Similarity: 73.15% Conservative: 0
Best Local Similarity: 73.15% Mismatches: 1
Query Match: 96.34% Indels: 336
DB: 18 Gaps: 1
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US-09-493-480-6 (1-919) x US-10-280-576-3 (1-3768)

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Db 1 ATGGAGCTGGCGGCTTGTGGCGCTGGGGCTCTCTCGCCCTTGGCCCCCGGAGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
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QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGGACATGTCTCCGCCACCTCTACAGGGCTGGCAGGTGGTGCAGGAAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACTCACCCTACCTGCCCCAACATGCCAGCTGTCTCTCTGTCAGGATATCCAGGAGGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGTGTCTATCGCTCAACACCAAGTGGGAGGAGTCCCTGTCAGAGGCTGCGG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTCCGAGGCACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGCTGTAGACATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCCTCAACAATAACACCCCTGTGCAGGGGCTTCCCGAGGAGGCTTCCGGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAGAGCTTCACAGAGATCTTGAAGGAGGGGTCTTGATCCAGCGGAAACCCAG 480
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
Db 481 CTCTGCTACAGGACACGATTTGTGGAAGGACATCTTCCACAAGAACCAACACAGCTGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACCAACCCGCTCTCGGGCTTCCACCCCTGTCTCCGATGTGTAAAG 600
QY 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGTGGGAGAGAGATTCTGAGGATTTGTACAGAGCTGACGCGCATCTGTCT 660
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 661 GCCGTGGCTGTGGCGCTGCAAGGGGCCACTGCCCACTGACTGTGTCATGAGCAGTGT 720
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGGCTGACGCGGCCCAAGCACTCTGACTGTGCTGGCTGCCCTCCACTTCAACAC 780
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCACTGCCCGCCCTGTGTCCTTACCAACAGACAGACGTTT 840
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 841 TCCATGCCCAATCCCGAGGCGGTATACATTCGGGCGCCAGCTGTGTGACTGCTGCTGCC 900
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerIysProCysAlaArg	340	Db	2041	AAATCCGGAAGTACACGATGCGGAGACTGTGTGAGGAAACGAGACTGTGTGAGCCGCTG	2100
Db	961	GAGGTACACGACAGAGATGAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCCCCG	1020	QY	653	-----	653
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAen	360	Db	2101	ACACCTAGCGGAGCGATGCCCAACGAGCGCAGATGCGGATCCTGAAAAGAGACGGAGCTG	2160
Db	1021	GTGTGCTATGTGGCATGGAGCATTTGCGAGAGGTGAGGCGAGTTACCACTGCCAAT	1080	QY	653	-----	653
QY	361	IleGlnGluPheAlaGlyCysIysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	Db	2161	AGGAAGTGAAGGTGCTTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC	2220
Db	1081	ATCCAGAGCTTTGCTGGCTGCAAGAAGATCTTTGGGAGCTGGCATTTCTGCGGAGAGC	1140	QY	653	-----	653
QY	381	PheAspGlyAspProAlaSerAenThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400	Db	2221	CCTGATGGGGAGAAATGTGAAAATTCACGTGGCCATCAAAAGTTGTGAGGAAAAACACATCC	2280
Db	1141	TTTGATGGGGAGCCAGCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1200	QY	653	-----	653
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	Db	2281	CCCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGGCTCCCCA	2340
Db	1201	GAGACTCTGGAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGACAGCCTGCCT	1260	QY	653	-----	653
QY	421	AspLeuSerValPheGlnAenLeuGlnValIleArgGlyArgIleLeuHisAenGlyAla	440	Db	2341	TATGTCTCCGCTTTCTGGGCATCTGCGTCATCCACGGTGCAGCTGCTGACACAGACTT	2400
Db	1261	GACCTCAGCGTCTTCCAGAACCCTGCAAGTAATCCGGGAGCGAATCTGCACAATGGCGCC	1320	QY	653	-----	653
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460	Db	2401	ATGCCCTATGGCTGCCTCTTAGACCATGTCCGGGAAAAACCGCGGAGCCCTGGGCTCCCAG	2460
Db	1321	TACTCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGGAA	1380	QY	653	-----	653
QY	461	LeuGlySerGlyLeuAlaLeuIleHisHisAenThrHisLeuCysPheValHisThrVal	480	Db	2461	GACCTGTGAACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGAGGAGTGTGCGG	2520
Db	1381	CTGGGAGTGGACTGGCCCTCATCCACCATATACCCACCTCTGTCTCGTGCACAGGTG	1440	QY	653	-----	653
QY	481	ProTrpAspGlnLeuPheArgAenProHisGlnAlaLeuLeuHisThrAlaAenArgPro	500	Db	2521	CTCGTACACAGGGACTTGGCCGCTCGGAACGTGTGCTCAAGAGTCCCAACCATGTCAA	2580
Db	1441	CCCTGGGACAGCTCTTTCCGAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1500	QY	653	-----	653
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	Db	2581	ATTACAGACTTCGGGCTGGCTCGGCTGGTGGACATTTGAGGACACAGAGTACCATGCAGAT	2640
Db	1501	GAGGACAGTGTGTGGCGAGGGCTTGGCTTCCACCACTGTGGCGCCGAGGGCACTGC	1560	QY	653	-----	653
QY	521	TrpGlyProGlyProThrGlnCysValAenCysSerGlnPheLeuArgGlyGlnGluCys	540	Db	2641	GGGGCAAAGTGCCTCATCAAGTGGATGCGCTGGAGTCCATTCTCCGCGCGGTTCAAC	2700
Db	1561	TGGGTCCAGGGCCCAACCCAGTGTGTCAACTGCAGCCAGTTCTTTCGGGGCCAGAGTGC	1620	QY	653	-----	653
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAenAlaArgHisCys	560	Db	2701	CACCAGATGATGTGTGAGTTATNGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC	2760
Db	1621	GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCGAGGGAGTATGTGAATGCCAGGCATGT	1680	QY	653	-----	653
QY	561	LeuProCysHisProGluCysGlnProGlnAenGlySerValThrCysPheGlyProGlu	580	Db	2761	AAACCTTACGATGGGATCCCAGCCCCGAGATCCCTGACCTGCTGGAAAAGGGGAGCGG	2820
Db	1681	TTGCCGTGCCACCTGAGTGTGAGCCCCAGAATGGCTCAGTACCTGTTTGGACCGGAG	1740	QY	653	-----	653
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GenCore version 5.1.6
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Run on: August 3, 2005, 12:34:58 ; Search time 284.625 Seconds
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Ygapop 10.0 , Ygapext 0.5
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Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents NA.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3776	95.5	3768	2	US-08-356-786-1
3	3776	95.5	3768	4	US-09-811-115-2
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5	3776	95.5	4473	3	US-09-056-105-26
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7	3776	95.5	4473	4	US-09-441-411-5
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14	3632	91.9	2385	2	US-09-146-283-3	Sequence 3, Appli
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16	3632	91.9	2385	3	US-09-344-195-3	Sequence 2, Appli
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19	3205	81.1	3955	1	US-08-229-515A-14	Sequence 14, Appl
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23	1534	38.8	5532	2	US-09-676-610B-17	Sequence 17, Appl
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25	1451	36.7	5501	1	US-08-484-438-1	Sequence 1, Appli
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27	1435	36.3	4905	1	US-07-978-895-3	Sequence 3, Appli
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33	1412	35.7	5687	4	US-09-919-039-268	Sequence 268, App
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36	1032	26.1	1958	3	US-09-570-454-1	Sequence 1, Appli
37	1032	26.1	1958	4	US-09-867-521-1	Sequence 1, Appli
38	942	23.8	1593	3	US-09-676-610B-25	Sequence 25, Appl
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41	493	12.5	322	1	US-08-421-356-1	Sequence 1, Appli
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44	369.5	9.3	4149	2	US-08-737-715-1	Sequence 1, Appli
45	369.5	9.3	4723	4	US-09-023-655-1137	Sequence 1137, Ap

ALIGNMENTS

RESULT 1

US-08-625-101-1
; Sequence 1, Application US/08625101
; Patent No. 5869445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3768 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..3765
 ; US-08-625-101-1

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US-08-356-786-1
; Sequence 1, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3768
; OTHER INFORMATION: /note= "product = "cerB-b2""
US-08-356-786-1

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 2 Gaps: 1

US-09-493-480-7 (1-712) x US-08-356-786-1 (1-3768)

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QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
Db	61	GCAGACCAACCAAGTGTGCACCGGCACAGACATGAAGCTGGGCTCCCTGCCAGTCCCGAG	120
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrglnGlyCysGlnValGlnGlnGlyAsnLeu	60
Db	121	ACCCACCTGGACATGCTCCGCCACCTCTACCAAGGCTGCAGGTGGTGGAGGAAACCTG	180
QY	61	GluLeuThrTyrlleuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal	80
Db	181	GAACCTCACCTACTGCCACCAATATGCAGCTGTCTCTCTCGAGGATATCCAGAGGTG	240
QY	81	GlnGlyTyrlleuValleuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	241	CAGGGCTAGCTCATCTCATCTCACACCAAGTGAGGCAGTCCCACCTGCAGAGGCTGGG	300
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrlleuAlaValleuAspAsnGly	120
Db	301	ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGACAAATGGA	360
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	361	GAACCCGCTGAACATACCAACCCCTGTACAGGGGCTCCACAGAGGCTGGGAGCTG	420
QY	141	GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuIleGlnArgAsnProGln	160
Db	421	CAGCTTCGAAGCTCACAGAGATCTTTGAAGGAGGGTCTTGATCCAGCGGAACCCCCAG	480
QY	161	LeuCysTyrlleuAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180
Db	481	CTCTGTACACGAGACAGATTTGTGGAAGGACATCTTCCACAAGAACCAACAGCTGGCT	540
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
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QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysHisGlnGlnCys	240
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QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	721	GCTGCCGGTGCACGGGCCCAAGCACTCTGACTGCCTGGCTGCTCCACCTTCAACCCAC	780
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrlleuAsnThrAspThrPheGlu	280
Db	781	AGTGGCATCTGTGAGCTGACCTGCCAGCCCTGGTCACTACACACACACACACGCTTTGAG	840
QY	281	SerMetProAsnProGluGlyArgTyrlleuPheGlyAlaSerCysValThrAlaCysPro	300
Db	841	TCCATGCCCAATCCCGAGGGCCGATATACATTCGGCGCCAGCTGTGTGACTGCCTGTGCC	900
QY	301	TyrAsnTyrlleuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	901	TACAACTACTTCTACGAGAGCTGGGATCTGTGACCCCTGTGTGCCCTGTCACAAACCA	960
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
Db	961	GAGGTGCACAGCAGAGGATGGAACACAGCGGTGTGAGAAAGTGACAGAGCCCTGTGCCCGA	1020
QY	341	ValCysTyrlleuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
Db	1021	GTGTGCTATGTGGCTGGGACACTTGCAGAGGTTGAGGGCATTTACAGTGCACAT	1080
QY	361	IleGlnGlnPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1081	ATCCAGGAGTTTGTGGCTGCAGAGAGATCTTTTGGAGGCTGGCATTTCTGCGGAGAGC	1140
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
Db	1141	TTTGTATGGGACCCAGCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1200
QY	401	GluThrLeuGluGluIleThrGlyTyrlleuTyrlleuSerAlaTrpProAspSerLeuPro	420
Db	1201	GAGACTCTGGAAAGAGATCACAGTTTACCTATATCATCTCAGCATGGCCGACAGCCTGCCT	1260
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
Db	1261	GAACCTCAGGCTCTTCAGAACCTGCAGTAATCCGGGAGCAATCTGCACAAATGGCGCC	1320
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
Db	1321	TACTCGCTGACCTGCAAGGGCTGGCATCAGCTGGCTGGGCTGCCTCACTGAGGGAA	1380
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
Db	1381	CTGGCAGTGGACTGGCCCTCATCCACCAATACACCCACCTCTGCTTCGTGCACACGGTG	1440
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
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QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
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Db	1621	GTGGAGGATGCGGAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT	1680
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
Db	1681	TTGCGCTGCCACCTTGAGTGTGAGCCCAAGATGGCTCAGTGCACCTGTCTTGGACCGGAG	1740
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrlleuAspProPheCysValAlaArgCys	600
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QY	601	ProSerGlyValLysProAspLeuSerTyrlleuTrpLysPheProAspGluGlu	620
Db	1801	CCCAGCGTGTGAACCTGACCTCTCTACATGCCCATCTGGAGTTTCCAGATGAGGAG	1860
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys	640
Db	1861	GGCGCATGCCAGCTTGGCCCATCAACTGACCCACTCTCTGTGTGGACCTGTGATGACAAG	1920
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	1921	GGCTCCCCCGGAGCAGAGAGCCCTCTGACGTCCATCATCTCTGCGGTGGTGTGGC	1980
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Db	1981	ATTCTGCTGCTGCTGCTTGGGGGTGGTCTTTGGGATCTTCATCAAGCGACGGCAGCAG	2040
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RESULT 3

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US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
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; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-811-115-2
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Alignment Scores:

Pred. No.:	0	Length:	3768
Score:	3776.00	Matches:	712
Percent Similarity:	67.94%	Conservative:	0
Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
DB:	4	Gaps:	1

US-09-493-480-7 (1-712) x US-09-811-115-2 (1-3768)

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Db	61	GGGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGGCGCTCCCTGCCAGTCCCGAG	120
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
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QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
Db	181	GAACCTACCTACTGCGCCCAATGCCAGCCTGTCTCTCTCCAGGATATCCAGGAGGTG	240
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
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QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys	240
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QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
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QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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RESULT 4
US-09-048-804-1
; Sequence 1, Application US/09048804
; Patent No. 5968748
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
; HUMAN HER-2 EXPRESSION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,804
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Leggaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4473 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; ANTI-SENSE: No
US-09-048-804-1

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 2 Gaps: 1

US-09-493-480-7 (1-712) x US-09-048-804-1 (1-4473)

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Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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RESULT 5

US-09-056-105-26
; Sequence 26, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221

! CURRENT APPLICATION NUMBER: US/09/056.105
! CURRENT FILING DATE: 1998-04-06
! EARLIER APPLICATION NUMBER: 60/043.467
! EARLIER FILING DATE: 1997-04-10
! NUMBER OF SEQ ID NOS: 35
! SOFTWARE: FastSeq for Windows Version 3.0
! SEQ ID NO 26
! LENGTH: 4473
! TYPE: DNA
! ORGANISM: Homo sapiens
US-09-056-105-26

Alignment Scores:

Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 3 Gaps: 1

US-09-493-480-7 (1-712) x US-09-056-105-26 (1-4473)

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DB 235 GCGAGCACCAGGTGCACCGGCACAGACATGAAGCTGGGCTCCCTGCCAGTCCCGAG 294
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QY 221 AlaGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
DB 835 GCGGGTGGCTGTGCGGCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 894
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 895 GCTGCCGGCTGCAGGGGCCCAAGACCTCTGACTGCTGCCCTGCCCTCCACTTCAACCCAC 954

QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 955 AGTGGCATCTGTAGCTGCACCTGCCAGCCCTGGTACCTACAAACACAGACACGTTTGAG 1014
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 1015 TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGCGCCAGCTGTGTGACTGCGCTGCC 1074
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QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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RESULT 6
US-09-663-834A-3
; Sequence 3, Application US/09663834A
; Patent No. 6613567
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
; FILE REFERENCE: RTS-0033
; CURRENT APPLICATION NUMBER: US/09/663,834A
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175) ... (3942)
US-09-663-834A-3

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-7 (1-712) x US-09-663-834A-3 (1-4473)

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Db 235 GCGAGCACCAAGTGTGCACCGCACACATGAAGTGTGGGCTCCCTGCCAGTCCCGAG 294
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyGlnGlyCysGlnValValGlnGlnGlnLeu 60
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QY 81 GlnGlyTyValLeuLeuAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
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RESULT 7
US-09-441-411-5
; Sequence 5, Application US/09441411
; Patent No. 6734172
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5
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Db 2455 CCCAAAGCCAAACAAAGAAATCTTTAGACGAAGCATACGTGATGGCTGTGTGGGCTCCCA 2514
QY 653 ----- 653
Db 2515 TATGTCTCCCGCTTCTTGGGCATCTGCCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2574
QY 653 ----- 653
Db 2575 ATGCCCTATGGCTGCCTCTTTAGACCATGTCTCGGAAAAACCGCGAGACGCTGGGCTCCAG 2634
QY 653 ----- 653
Db 2635 GACCTGCTGNACTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCGG 2694
QY 653 ----- 653
Db 2695 CTGCTACACAGGAGACTTGGCGCTCGGAACGTGCTGTCAAGAGTCCCAACCATGTCAAA 2754
QY 653 ----- 653
Db 2755 ATTACAGACTTGGGGTGGCTCGGCTGCTGGAATTGACGAGACAGAGTACCATGCGAGAT 2814
QY 653 ----- 653
Db 2815 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCCGCGGGTTCACC 2874
QY 653 ----- 653
Db 2875 CACCAGAGTATGTGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2934
QY 653 ----- 653
Db 2935 AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGTGTGGAAGGGGAGCGG 2994
QY 653 ----- 653
Db 2995 CTGCCCCAGCCCCCTCTGCACCATTTGATGTCTACATGATCATGTTCAATGTTGGATG 3054
QY 653 ----- 653
Db 3055 ATTGACTCTGAATGTCCGCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 3114
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3115 AGGACCCCCAGCGCTTTTGTGTCATCCAGAATGAGGACTTGGGCCCGACGACGCTTGTG 3174
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3175 GACAGACCTTCTACCGCTCACTGCTGGAGGACATGACATGGGGACCTTGGTGGATGCT 3234
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3235 GAGGAGTATCTGTGTACCCAGCAGGGCTTCTTCTGTCCAGACCTTGCCTCCGCGCGCTGG 3294
QY 705 GlyMetValHisHisArgHisArg 712
Db 3295 GGCATGTCACACACAGGCACGCGC 3318
RESULT 8
US-08-229-515A-9
; Sequence 9, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: NEEDLE & ROSENBERG PC
 STREET: 127 Peachtree Street, Suite 1200
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: usa
 ZIP: 30303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/229,515A
 FILING DATE: 19 APR 1994
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: PERRYMAN, DAVID G
 REGISTRATION NUMBER: 33,438
 REFERENCE/DOCKET NUMBER: 1414.608
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-688-0770
 TELEFAX: 404-688-9880

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4530 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-229-515A-9

Alignment Scores:

Pred. No.: 0 Length: 4530
 Score: 3776.00 Matches: 712
 Percent Similarity: 67.94% Conservative: 0
 Best Local Similarity: 67.94% Mismatches: 0
 Query Match: 95.50% Indels: 336
 DB: 1 Gaps: 1

US-09-493-480-7 (1-712) x US-08-229-515A-9 (1-4530)

Qy 1 MetGluLeuAlaLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20
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 Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
 Db 211 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTCGCGCTCCCTGCCAGTCCCGAG 270
 Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
 Db 271 ACCACCTGGACATGCTCGCCACCTCTACCGAGGCTGCAGGTGGTCAGGGGAACCTG 330
 Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
 Db 331 GAACTCACCTACTGCCCCCAATGCCAGCTGTCTCTCCAGGATATCCAGAGGTG 390
 Qy 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
 Db 391 CAGGGCTACGTGCTCATCGCTCACACCAAGTGAGCGAGGTCCCACTGCAGAGGCTGGG 450
 Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
 Db 451 ATTGTGGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGACAACTGA 510
 Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyClyLeuArgGluLeu 140
 Db 511 GACCCGCTGAACAATACCACTGTGCACAGGGGCTCCCGAGAGGCTGGGGAGCTG 570
 Qy 141 GlnLeuArgSerLeuThrGlnIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
 Db 571 CAGCTTCGAAGCTTCACAGAGATCTTTGAAGAGGGGTCTTATCCAGCGGAACCCCGAG 630

Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla 180
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 Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
 Db 691 CTCACACTGATAGACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAAG 750
 Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
 Db 751 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGGATTGTGAGAGCTGACGGCACTGTCTGT 810
 Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
 Db 811 GCCGTGGCTGTGCCCGCTGCAAGGGCCACTGCCCACTGCTGCTGCCACTGAGCAGTGT 870
 Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
 Db 871 GCTGCCGCTGCACGGGCCCAAGCACTCTGACTGCTGCTGGCTGCCCTCCACTTCAACCCAC 930
 Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
 Db 931 AGTGCATCTGTGAGCTGCACTGCCCGCCCTGGTCACTCAACACACACACAGCTTTGAG 990
 Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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 Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysAspProCysAlaArg 340
 Db 1111 GAGGTGACAGCAGAGATGGAACACAGCGGTGTGAGAGTGCAGCAGCCCTGTGCCCGA 1170
 Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
 Db 1171 GTGTCTATGTCTGGGCATGGAGCACTTTCGAGAGGTGAGGGCAGTTACCAAGTGCCAAT 1230
 Qy 361 IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
 Db 1231 ATCCAGGAGTTTGTCTGGCTGCAAGAGATCTTTGGAGGCTTGGCATTTCTGCCGAGAGC 1290
 Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
 Db 1291 TTTGATGGGACCCAGCCTCCAACTGCCCGCTCCAGCCAGCAGCAGCTCCAGTGT 1350
 Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
 Db 1351 GAGACTCTGGAAGAGATCACAGTTTACCTATATACATCTCAGCATGCGCGACAGCTGCCT 1410
 Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
 Db 1411 GACCTCAGCGCTTTCAGAACCTGCAAGTAATTCGCGGACGAATTCGCACAATGGCGCC 1470
 Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
 Db 1471 TACTCGCTACCTGCAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTAGAGGAA 1530
 Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
 Db 1531 CTGGCAGTGGACTGGCCCTCATCCACCAATACACCCACTCTGCTTCGTGCACACGGTG 1590
 Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
 Db 1591 CCCTGGGACCACTCTTTGGAAACCCGACCAAGCTCTGCTCCACTCCCAACCGGCCA 1650
 Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
 Db 1651 GAGGACAGTGTGTGGCGAGGGCTTGGCTGCCACAGCTGTGGCCCGCGGCACTGC 1710
 Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540

Db 1711 TGGGGTCCAGGGCCACCCAGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC 1770
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaAtrgHisCys 560
Db 1771 GTGGAGGATGCCAGTACTGCAGGGCTCCACAGGAGTATGTGAATGCAGGCACTGT 1830
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1831 TTGCGTGCACCCCTGAGTGTGAGCCCAAGATGGCTCAGTGACCTGTTTTGGACCGAG 1890
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrIysAspProPheCysValAlaAtrgCys 600
Db 1891 GCTGACAGAGTGTGGGCTGTGCCACTATAGACCCCTCCCTTCGCGTGGCCGCTGC 1950
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1951 CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAATTTCCAGATGAGGAG 2010
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db 2011 GGGCATGCCAGCCTTGCCCACTCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAAG 2070
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 2071 GGCTGCCCCCGCAGCAGAGCAGCCCTCTGACGTCCATCGTCTCTGCGGTGGTTGGC 2130
QY 653 ----- 653
Db 2131 ATTCTGCTGTGTGCTTGGGGTGGTCTTTGGGATCCTCATCAAGCAGCGCAGCAG 2190
QY 653 ----- 653
Db 2191 AAGATCCGAAGTACACGATGCGGAGACTGCTGCAGGAACGGAGCTGTGTGGAGCCGCTG 2250
QY 653 ----- 653
Db 2251 ACACCTAGCGAGCGATGCCCAACAGCGCAGATCGGATCCTGAAAGACGGAGCTG 2310
QY 653 ----- 653
Db 2311 AGAAGGTGAAGTGTGTGATCTGGCGCTTTTGGCAGCTGTACAGGGCATCTGGATC 2370
QY 653 ----- 653
Db 2371 CCTGATGGGAGAATGTGAAATTTCCAGTGGCCATCAAACTGTGTAGGGGAAACACATCC 2430
QY 653 ----- 653
Db 2431 CCCAAAGCCAAAGAAATCTTAGAGAAAGCATACGTGATGCTGTGTGGGCTCCCCA 2490
QY 653 ----- 653
Db 2491 TATGTCTCCGCCCTTCTGGGCATCTGCTGACATCCACGGTGCAGCTGTGTGACACAGCTT 2550
QY 653 ----- 653
Db 2551 ATGCCCTATGCTGCTCTTTAGACCATGTCCGGGAAACCGCGGACGCTGGCTCCAG 2610
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Db 2671 CTCGTACACAGGACTTGGCCGCTCGGAACGTGCTGCTCAAGAGTCCCAACCATGTCAAA 2730
QY 653 ----- 653
Db 2731 ATTACAGACTTGGGCTGGCTCGGCTGCTGATGATGATGATGATGATGATGATGATGAT 2790
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Db 2791 GGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGCTTACC 2850
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Db 2851 CACCAGAGTATGTGTGGAGTATGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC 2910
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Db 3031 ATTGACTCTCAATGTGCGCCAGATTCGGGAGTGTGTGTGATTTCTCCGCGATGGCC 3090
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 3091 AGGGACCCCGAGCGCTTTGTGGTCAATCCAGAAATGAGGACTTGGGCCCGAGCCAGTCCCTTG 3150
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3151 GACAGCACCTTTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCT 3210
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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Db 3271 GGCAATGTCACACAGCAGCCAGCCG 3294

RESULT 9
US-08-645-865-9
; Sequence 9, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPlastic DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-645-865-9

Alignment Scores:

Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 1 Gaps: 1

US-09-493-480-7 (1-712) x US-08-645-865-9 (1-4530)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
DB 211 GCGAGCACCAAGTGTGACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG 270
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
DB 271 ACCCACTTGGACATGCTCGCCACCTCTTACCAAGGCTGCCAGGTGGTGAGGAAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnVal 80
DB 331 GAACCTCACCTACTGCCACCAATGCCAGCTGTCTTCTCTCGAGGATATCCAGAGGTG 390
QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
DB 391 CAGGGCTACGTCTCATCGCTCACCAACCAAGTGAGGAGGTGCCACTGTCAGAGGTGGG 450
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspGln 120
DB 451 ATTGTGCGAGGACCCAGCTCTTTGAGGACAATATGCCCTTGGCCGTGTAGCAATGGA 510
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
DB 511 GACCGCTGAACAATACCACCCCTGTACAGGGGCTTCCCAAGGAGGCTGCGGAGGTG 570
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
DB 571 CAGCTTCGAAGCCTCACAGAGATCTTGAAGAGGGGTCTTGATCAGCGGAACCCAG 630
QY 161 LeuCysTyrGlnAspThrIleLeuTrrpLysAspIlePheHisLeuAsnGlnLeuAla 180
DB 631 CTCGTCTACGAGCACGATTTTGTGAGAGACATCTTCCAAAGAACCAACAGCTGGCT 690
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
DB 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTCTCCGATGTGAAG 750
QY 201 GlySerArgCysTrrpGlySerSerGluAspCysGlnSerLeuThrArgThrValCys 220
DB 751 GGTCTCCGCTGTGGGAGAGAGATTCTGAGGATTGTGAGAGCTGACAGCGCTACTGTCTGT 810
QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
DB 811 GCGGTGGCTGTGGCGCTGCAAGGGCCACCTGCCCACTGACTGTCTGCCATGAGCAGTGT 870
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
DB 871 GCTGCCGCTGCACGGGCCCCAAGCACCTGACTGCTGCCCTGGCTGCCCTTCAACCCAC 930
QY 261 SerGlyIleCysGlnLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
DB 931 AGTGGCATCTGTGAGCTGACCTGCCAGCCCTGGTCAACCTACCAACACACACACGTTTGAG 990
QY 281 SerMetProAsnProGluGlnValArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
DB 991 TCCATGCCCAATCCCGAGGGCCGTATACATTGGGGCCGAGCTGTGTACTGCCCTGTCCC 1050
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320

DB 1051 TACAACTACCTTTTCTACGGACGTGGATCTCGACCCCTCGTCTGCCCTCGCACACCAA 1110
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysPrrCysAlaArg 340
DB 1111 GAGGTGACAGCAGAGATGGAACACAGCGGTGTGAGAAGTGCAGGAAGCCCTGTGCCGA 1170
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
DB 1171 GTGTCTATGTCTGGGCATGGAGCACCTTGCAGAGGTGAGGGCAGTTACCAAGTGCAT 1230
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
DB 1231 ATCCAGGAGTTTGTGTGGCTGCAAGAAGATCTTTTGGAGGCTCGCATTTCTGCCGAGAGC 1290
QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
DB 1291 TTTGATGGGGACCCAGCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1350
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrrpProAspSerLeuPro 420
DB 1351 GAGACTCTGGAAAGAGATCACAGTTACTTATACATCTCAGCATGGCCGAGCAGCTGCCT 1410
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisshenGlyAla 440
DB 1411 GACCTCAGCGTCTTCCAGAACCTGCAAGTAATCCGGGAGCAATCTGCACAATGGCGCC 1470
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrrpLeuGlyLeuArgSerLeuArgGlu 460
DB 1471 TACTCGCTGACCTTCAAGGGCTGGGCATCAGCTGGCTGGGGCTCGCTCAGTAGGGAA 1530
QY 461 LeuGlySerGlyLeuAlaLeuIleHisshenThrHisLeuCysPheValHisThrVal 480
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QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisshenAlaAsnArgPro 500
DB 1591 CCCTGGGACCACTCTTTCCGAACCCGACCAAGCTCTGCTCCACACTGCCAACCGCCA 1650
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QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
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QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1771 GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1830
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
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DB 1891 GCTGACGAGTGTGGCTGTGGCCACTATAAGGAGCCCTCCCTTCTGCGTGGCCGCTGC 1950
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProLleTrrpLysPheProAspGluGlu 620
DB 1951 CCCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 2010
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
DB 2011 GCGCATGCCAGCTTGGCCCATCAACTGACCCCACTCTCTGTGTGAGCTGTGATGACAAG 2070
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
DB 2071 GGCTGCCCCGCGACGAGAGCCAGCCCTCTGAGCTCCATCGTCTCTGCGGTGGTTGGC 2130
QY 653 ----- 653

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Db 2131 ATTCTGCTGTCGTGGTCTTTGGGGTGGTCTTTGGGATCCTCATCAAGCAGCGCAGCAG 2190
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Db 2191 AAGATCCGAAGTACACGATGCGGAGACTGCTGCAGGAACGGAGCTGGTGAGCCGCTG 2250
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Db 2251 ACACCTAGCGAGCGATGCCCAACAGCGCAGATCGGATCCTGAAAGAGACGAGCTG 2310
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Db 2311 AGGAAGTGAAGTGTGGATCTGGCGCTTTTGGCACACTTACAAGGGCATCTGGATC 2370
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Db 2371 CCTGATGGGAGAATGTGAAAATTCAGTGGCCATCAAAGTGTGAGGAAACACATCC 2430
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Db 2431 CCNAAGCCAAACAAAGAAATCTTAGAGAAAGCATACGTGATGCTGGTGTGGGCTCCCA 2490
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Db 2491 TATGCTCCCGCCTTCTGGGCATCTGCCTGACATCCACGGTGAGCTGTGACACAGCTT 2550
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Db 2551 ATGCCCTATGGCTCTTAGACCATGTCCGGGAAACCGCGGACGCTGGGCTCCAG 2610
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Db 2611 GACCTGCTGAATGGTGTATGAGATTGCCAAGGGGATGAGTACCTGGAGGATGTGCGG 2670
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Db 2671 CTGTTACACAGGACTTGGCCGCTCGGAACGTGCTGGAAGTCCCAACCATGTCAA 2730
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Db 2731 ATTACAGACTTCCGGTGGCTCGGCTCGTCTGGACATTGACGAGACAGTACCATGCAGAT 2790
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Db 2791 GGGGCAAGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCCGCGGTTCAAC 2850
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Db 2851 CACCAGATGATGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGCTTTTGGGGCC 2910
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Db 2911 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTGGAAAGGGGAGCGG 2970
Qy 653 -----
Db 2971 CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGTGTTCAAATGTGGATG 3030
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Db 3031 ATTGACTCTGAATGTGGGCCAAGATCCCGGAGTGTGGTGTCTGAAATTCCTCCCGCATGGCC 3090
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Db 3091 AGGGACCCCGCGCTTTGTGGTTCATCCAGAATGAGGACTTGGGCCAGCCAGCTCCCTTG 3150
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RESULT 10
US-09-167-322-4
; Sequence 4, Application US/09167322
; Patent No. 6365151
; GENERAL INFORMATION:
; APPLICANT: Allegheny University of the Health
; Sciences, Halpern, Michael S.
; England, James M.
; TITLE OF INVENTION: CANCER VACCINE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seidel, Gonda, Lavorna & Monaco, P.C.
; STREET: Suite 1800, Two Penn Center Plaza
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/167,322
; FILING DATE: 07-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/00582
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 7933-33 PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4530 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-167-322-4

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 3 Gaps: 1

US-09-493-480-7 (1-712) x US-09-167-322-4 (1-4530)
Qy 1 MetGluLeuAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuProProGlyAla 20
Db 151 ATGGAGCTGGCGCTTGTGCGCTGGGGCTCCTCTGCGCCCTTGTGCCCCCGGAGCC 210
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLeuLeuArgLeuProAlaSerProGlu 40
Db 211 GCGAGACCAAGTGTGCACCGGCACAGACATGAAGCTCGGCTCCTGCGCAGTCCCGAG 270
Qy 41 ThrHisLeuAspMetLeuHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 271 ACCACCTGGACATGCTCGCCACCTCTTACACAGGGCTGCAGGTGGTGACGGGAACCTG 330
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspTleGlnGluVal 80
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Db	331	GAACTCACCTACTGTCGCCACCAATGCCAGCTGTCTCTCTGTCAGGATATCCAGGAGGTG	390	Db	1411	GACCTCAGCGTCTTCCAGAACTTCGCAAGTAATCCGGGACGAATTCCTGCACAAATGGCGCC	1470
Qy	81	GInGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuCInArgLeuArg	100	Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
Db	391	CAGGGCTAGCTGCTCATCGCTCACACCAAGTGAGGCAGGTCCCATCTGCAGAGGTGCGG	450	Db	1471	TACTCGCTGACCCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTCAGGGGAA	1530
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120	Qy	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
Db	451	ATTGTGCGAGGCACCCAGCTCTTTGAGGACACTATGCCCTGGCCGTGTAGACATGGA	510	Db	1531	CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTGGTCACACGGTG	1590
Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140	Qy	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
Db	511	GACCCGCTGAACAATAACACCCCTGTGCACAGGGCCCTCCCCAGGAGGCTCGCGGAGCTG	570	Db	1591	CCCTGGGACCACTCTTTCCGAAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1650
Qy	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160	Qy	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
Db	571	CAGCTTCGAAGCTTCACAGAGATCTTTGAAAGAGGGGTCTTGATCCAGCGGAACCCCCAG	630	Db	1651	GAGGACGAGTGTGGGCGAGGGCTGGCCCTGCCACCAGCTGTGCCCGGAGGGCACTGC	1710
Qy	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla	180	Qy	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	631	CTCTGCTACAGGACACGATTTTGTGGAAGGACATCTTCCACAGAACCAACAGCTGGCT	690	Db	1711	TGGGGTCCAGGGCCACCCAGCTGTCTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTG	1770
Qy	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200	Qy	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
Db	691	CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAA	750	Db	1771	GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCCAGGGAGTATGTGAATGCCAGGCACTGT	1830
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Db	751	GGCTCCCGCTGTGGGAGAGAGATTCTGAGGATTTGTACAGAGCTGACGGCGCATCTGTGT	810	Db	1831	TTGCCGTGCCACCTGTAGTGTGAGCCCGAGAAATGGCTCAGTACCTGTTTGGACCGGAG	1890
Qy	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240	Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys	600
Db	811	GCGGTGGTGTGCCGCTGCAAGGGCCACTGCCCACTGACTGTGCTGCCATGAGCAGTGT	870	Db	1891	GCTGACCACTGTGTGGCTGTGCCCTGTGCCCACTATAAGGACCCTCCCTTCTGGTGGCCGCTGC	1950
Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260	Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
Db	871	GCTGCCGGTGCACGGGCCCAAGCACTCTGACTGCTGCTGGCTGCCCTCCACTTCAACCA	930	Db	1951	CCCAGCGGTGTGAACACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	2010
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280	Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys	640
Db	931	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTGCACCTACCAACACAGACACGTTTGAG	990	Db	2011	GGCGCATGCCAGCTTGCCCATCAACTCAACTGCACCCACTCTGTGTGGACTGTGATGACAAG	2070
Qy	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300	Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
Db	991	TCCATGCCCAATCCCAGGGCCGGTATACATTCGGGCCAGCTGTGTGACTGCTGCTGCC	1050	Db	2071	GSGTSCCCCGCGACGACGAGAGCCAGCCCTCTGAGCTCCATCGTCTCTGCGGTGGTTGSG	2130
Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320	Qy	653	-----	653
Db	1051	TACAACACTACTTCTACGGACGTGGGATCTGTGACCCCTGCTGTGCCCTCGTCACAACCAA	1110	Db	2131	ATTCTGCTGTCGTGTCGTCTTGGGGGTGGTCTTTTGGGATCTCTCATCAAGCGACGGCAGCAG	2190
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	Qy	653	-----	653
Db	1111	GAGGTGACAGCAGAGATGGAACACACAGCGGTGTGAAGTGCAGCAAGCCCTGTGCCCGA	1170	Db	2191	AAGATCCGGAAGTACACGATGCGGAGACTGTGTGAGGAAACGGAGCTGTGTGAGCGCGCTG	2250
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	Qy	653	-----	653
Db	1171	GTGTGCTATGTCTGGGCATGAGACACTTTCGAGAGGTGAGGGCAGTTACCACTGCCCAT	1230	Db	2251	ACACCTAGCGGAGCGATGCCCAACCGAGCGCAGATGCCGATCCTGAAAGAGACGGAGCTG	2310
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	Qy	653	-----	653
Db	1231	ATCCAGAGTTTGTGCTGGCTGCAAGAAGATCTTTGGGAGCCTGGCATTTCTGCGGAGAGC	1290	Db	2311	AGGAAGTGAAGGTGCTTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC	2370
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe	400	Qy	653	-----	653
Db	1291	TTTGATGGGGACCCAGCCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCAAGTGTGT	1350	Db	2371	CCTGATGGGGAGATGTGAAAATTCCAGTGGCCATCAAAAGTGTGGGAAACACATCC	2430
Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	Qy	653	-----	653
Db	1351	GAGACTCTGGAAGAGATCAGAGTTACCTATACATCTCAGCATGGCCGACAGCCTGCCT	1410	Db	2431	CCCAAAGCCAAACAAGAAATCTTAGACGAAGCATACGTGATGGTGGTGGCTCCCCA	2490
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	Qy	653	-----	653
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QY 665 AspSerThrPheTyrArgSerLeuGluAspMetGlyAspLeuValAspAla 684
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QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
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RESULT 11

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US-09-527-487-1
; Sequence 1, Application US/09527487
; Patent No. 6528060
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles
; TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
; FILE REFERENCE: 126881309200
; CURRENT APPLICATION NUMBER: US/09/527,487
; CURRENT FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(3915)
US-09-527-487-1
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Alignment Scores:

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Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1
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US-09-493-480-7 (1-712) x US-09-527-487-1 (1-4530)

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Db 151 ATGGAGCTGGCGGCTTGTGCCCTGGGGCTCTCTCTCGCCCTTTCGCCCGGAGCC 210
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
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QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 271 ACCCAGCTGGACATGTCTCGCCACCTCTACAGGGCTGCCAGGTGGTGCAGGAAACCTG 330
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 331 GAACTCACCTTACCTGCGCCCAATGCCAGCCTGTCTCTCTGCGAGGATATCCAGGAGGTG 390
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
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QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
Db 511 GACCCCTGAAACAATAACACCCCTGTCCAGAGGGCTTCCCGAGGAGGCTTGGGGAGCTG 570
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
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QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
Db 631 CTCTGCTACAGGACACGATTTTGTGGAAGGACATCTTCCACAAGAACCAACAGCTGGCT 690
QY 181 LeuThrIleLeuAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 691 CTCACACTGATAGACCAACCCCTCTCGGGCTTGCACCCCTGTCTTCTCCGATGTGTAAG 750
QY 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
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QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 931 AGTGGCATCTGTGAGCTGCACTGCCCGAGCCCTGGTCACTACCAACACAGACAGATTGAG 990
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 991 TCCATGCCCAATCCCGAGGGCGGTATACATTGCGGCCAGCTGTGTGACTGCTGCTGCC 1050
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
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Dd	1051	TACAACTACCTTTCTACGACGTGGGATCTGACACCTCGTCTGCCCCCTGCACACCAA	1110	Qy	653	-----	653
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340	Dd	2191	AGATCCGGAAGTACACGATCGGGAGACTGTGTCAGGAAACGGAGCTGTGTGGAGCGCTG	2250
Dd	1111	GAGGTGACAGCAGAGATGAAACACAGCGGTGTGAAGTGCAGACGCCCTGTGCCGA	1170	Qy	653	-----	653
Qy	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360	Dd	2251	ACACCTAGCGGAGCGATGCCCAACCAAGCGCAGATGCGGATCCTGAAAGACAGGAGCTG	2310
Dd	1171	GTGTGCTATGTCTGGGCTGGGACATTCGCGAGAGTGCAGGCGAGTTACCAAGTGCCAA	1230	Qy	653	-----	653
Qy	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380	Dd	2311	AGGAAGTGAAGTCTTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC	2370
Dd	1231	ATCCAGAGATTTGCTGGCTGCAAGAGATCTTTGGGAGCTGGCAATTTCTGCCGAGAGC	1290	Qy	653	-----	653
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe	400	Dd	2371	CCTGATGGGAGAAATGTGAAAATTCAGTGGCCATCAAAGTGTGAGGGAACACATCC	2430
Dd	1291	TTTGATGGGAGCCAGCCCTCCAACTGCGCCGCTCCAGCCAGAGCAGCTCCAAGTGTTT	1350	Qy	653	-----	653
Qy	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420	Dd	2431	CCCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGCTGGTGTGGCTCCCCA	2490
Dd	1351	GAGACTCTGGAAGAGATCACAGGTTACCTATACATCTCAGCATGGCGGACAGCCTGCCT	1410	Qy	653	-----	653
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440	Dd	2491	TATGTCTCCGCTTCTTGGGCATCTGCCTGACATCCAAGTGCAGCTGGTGCACACAGCTT	2550
Dd	1411	GACCTCAGCGTCTTCAGAACCTGCAAGTAATCCGGGAGCGAATTCGACAAATGGCGCC	1470	Qy	653	-----	653
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460	Dd	2551	ATGCCCTATGGTGCCTCTTAGACCATGTCCGGGAAACCGCGAGCGCTGGGCTCCAG	2610
Dd	1471	TACTCGCTGACCTCGACGGCTGGGCATCAGCTGGCTGGGCTGGCTCACTGAGGGAA	1530	Qy	653	-----	653
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Dd	1531	CTGGGAGTGGACTGGCCCTCATCCACCATAACCCACCTCTCTGCTTCGTGCACACGGTG	1590	Qy	653	-----	653
Qy	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500	Dd	2671	CTCGTACACAGGGAATTTGGCCGCTCGGAACGTGTGTGTCGAAGAGTCCCAACCATGTCAA	2730
Dd	1591	CCCTGGGACAGCTCTTTCCGAAACCGCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA	1650	Qy	653	-----	653
Qy	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520	Dd	2731	ATTACAGACTTCGGGCTGGCTGGCTGGTGCAGATTTGACGAGACAGAGTACCATGCAGAT	2790
Dd	1651	GAGGACAGTGTGTGGCGGAGGCGCTGGCCCTGCCACAGCTGTGGCGCCGAGGGCACTGC	1710	Qy	653	-----	653
Qy	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540	Dd	2791	GGGGCAAAGTGCCTCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTCAAC	2850
Dd	1711	TGGGTCCAGGCCCCACCCAGTGTGTCAACTGCAGCCAGTCTCTTCGGGGCCAGAGTGC	1770	Qy	653	-----	653
Qy	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560	Dd	2851	CACCAGTGTATGTGTGGAGTTATGGTGTGACTGTGTGGGAGCTGATGACTTTTGGGGCC	2910
Dd	1771	GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCAGGGAGTATGTGAATGCCAGGCACGTG	1830	Qy	653	-----	653
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Dd	1831	TTGCCGTGCCACCTGAGTGTGAGCCCCAGAAATGGCTCAGTACCTGTTTGGACGGAG	1890	Qy	653	-----	653
Qy	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600	Dd	2971	CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTATCATGATCATGTCAAATGTTGGATG	3030
Dd	1891	GCTGACCAAGTGTGGCCTGTGCCACTATAGGACCTCCCTCTCTGCGTGGCCCGCTGC	1950	Qy	653	-----	653
Qy	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProaspGluGlu	620	Dd	3031	ATTGACTCTGAATGCGCCAAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC	3090
Dd	1951	CCGAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTCGAAGTTTCCAGATGAGGAG	2010	Qy	654	-----	664
Qy	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys	640	Dd	3091	AGGAGCCCCCAGCGCTTTGTGTCATCCAGATGAGGACTTGGGCCACCGCATCCCTTG	3150
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Qy	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653	Dd	3151	GACAGACCTTCTACCGCTCACTGTGGAGGACGATGACATGGGGACCTGTGTGATGCT	3210
Dd	2071	GGCTGCCCGCGAGCAGAGACGACCCCTCTGACGTCCATCGTCTCTCGCGGTGGTGGC	2130	Qy	685	GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly	704
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Dd	2131	ATTCTGCTGGTCTGTGGGTGGTCTTTTGGGATCCTCATCAAGCGCAGCGCAGCAG	2190				


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QY 705 GlyMetValHisHisArgHisArg 712
Db 3271 GGCATGGTCCACCACAGCCACCGC 3294

RESULT 12
US-09-877-177A-11
; Sequence 11, Application US/09877177A
; Patent No. 6582919
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; TITLE OF INVENTION: and Correlation of Levels Thereof With Survival
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177A-11

Alignment Scores:
Pred. No.: 0 Length: 4530
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1

US-09-493-480-7 (1-712) x US-09-877-177A-11 (1-4530)

QY 1 MetGluLeuAlaLeuCysArgTgGlyLeuLeuAlaLeuProGlyAla 20
Db 151 ATGGAGCTGGGGCTTGTGCGCGCTGGGGGCTCTCTCTGCCCTCTTGGCCCCCGGAGCC 210

QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
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QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
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QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 331 GAACCTACCTACCTGCCCAACCAATGCCAGGCTGTCTCTCTGAGGATATCCAGGAGGTG 390

QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 391 CAGGGCTACGTCTATCGTCTACACCAAGTGCAGGAGTCCCACTGCAGAGGCTGGCG 450

QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 451 ATTGTGCGAGCACCCAGCTCTTTAGGACAACTATATGCCCTGGCGGTGTAGACAAATGGA 510

QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 511 GACCCGCTGAACAAATACACCCCTGTCCAGGGGCTCTCCCAAGAGGCTCTGCGGGAGCTG 570

QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 571 CAGCTTCGAGGCTTCACAGAGATCTTGAAGAGGGGTCTTTGATCCAGCGGAAACCCCGAG 630

QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 631 CTCTGCTACGAGACAGATTTTGTGAAGAGACATCTTCACAAAGAACCAACACAGCTGGCT 690

QY 181 LeuThrIleLeuAspThrAsnArgSerArgAlaCysHisAspProMetCysLys 200
Db 691 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCGACCCCTGTCTCCGATGTGTAAG 750

QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 751 GGCTCCCGCTGCTGGGGAGAGATTCTGAGGATTGTGAGAGCTGTGACGCGCTGTCTGT 810

QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 811 GCCGGTGGCTGTGCCCGCTGCACAGGGGCCACTGCCCACTGCTGCTGCTGCTGCTGCTGCT 870

QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 871 GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930

QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 931 AGTGGCATCTGTGAGCTGCACCTGCCCAGCCCTGGTCACTACCAACACAGACAGCTTTGAG 990

QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 991 TCCATGCCCAATCCCGAGGGCCGGTATACATTCGGGGCCAGCTGTGTGACTGTGCTGTCCC 1050

QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 1051 TACAACTACTTCTACGGACGTGGGATCTGTGACCCCTGTCTGCCCTGTCACCAACCAA 1110

QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 1111 GAGGTGCACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCGA 1170

QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1171 GTGTGCTATGGTCTGGGCATGGAGCACTTGCAGAGGTGAGGGCAGTTACAGTGGCCAA 1230

QY 361 IleGlnGluPheAlaGlyCysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1231 ATCCAGAGTTTGTGCTGCTGCAAGAAGATCTTTGGAGGCTTGCATTTCTTCCGGGAGGC 1290

QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1291 TTTGATGGGGACCCAGCCCTCCAACACTGCCCCGCTCCAGCCAGCAGCAGCTCCAAGTGT 1350

QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 1351 GAGACTCTGGAAGAGATCACAGGTTTACCTATATACATCTCAGCATGGCGGACAGCCTGCCT 1410

QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1411 GACCTCAGGCTCTTCCAGAACCTGCAGTAATCCGGGGAGCAATTTCTGCACATATGGGCC 1470

QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1471 TACTGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCACTGAGGGAA 1530

QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1531 CTGGGAGTGGAGCTGGCCCTCATCCACCAATAACACCCACTCTGCTTCTGTCACACGGTG 1590

QY 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
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QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGlnCys 540
Db 1711 TGGGGTCCAGGGGCCCAACCCAGTGTGTCAACTGCAGCAGTTCCTTCTGGGGCCAGGAGTGC 1770

QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1771 GTGGAGGAATGCCAGTACTTGCAGGGGCTTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1830
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QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
Db 1831 TTGCCGTGCCACCTGAGTGTAGCCGCCAGAGATGGCTGAGTACCTGTTTGGACCGGAG 1890
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
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QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1951 CCAGCGGTGTAAACCTGACCTCTCTATATGCCCATCTGGAAGTTTCCAGATGAGGAG 2010
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
Db 2011 GGGCATGCGAGCTTGCCCCATCACTGCACCCCACTCTGTGTGGACCTGATGACAG 2070
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Db 2071 GGCTGCCCGCGAGCAGAGACGACGCTCTGACGTCCATCGTCTCTGCGGTGGTTGGC 2130
QY 653 ----- 653
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QY 654 -----GlnAenGluAspLeuGlyProAlaSerProLeu 664
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QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
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QY 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
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QY 705 GlyMetValHisHisArgHisArg 712
Db 3271 GGCATGGTCCACCACGACGACCGC 3294
RESULT 13
US-09-811-115-1
; Sequence 1, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector Sequence
US-09-811-115-1
Alignment Scores:
Pred. No.: 0 Length: 9274
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 4 Gaps: 1
US-09-493-480-7 (1-712) x US-09-811-115-1 (1-9274)
QY 1 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 1791 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGTGCAGTCCCTGCCAGTCCCGAG 1850
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 1851 ACCCACCTGGACATCTCCGCCACCCTCTTACCAGGGCTGCAGGTGGTGCAGGGAACCTG 1910
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Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 1911 GAACCTCACTACCTGCCCCACCAATGCCAGCGCTGCTTCTTCCAGGATATCCAGAGAGTG 1970
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 1971 CAGGGCTACGTGCTCATGCTCACAAACCAAGTAGGAGAGTCCCACTGCAGAGGCTGGG 2030
Qy 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 2091 GACCCGCTGAACAATACACCCCTGTACAGGGGCTTCCCGAGGAGGCTGGGGAGCTG 2150
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyGlyValLeuIleGlnArgAsnProGln 160
Db 2151 CAGCTTCGAAGCTTCACAGAGATCTTGNAGGAGGGTCTTGTATCCAGCGGAACCCCGAG 2210
Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 2211 CTCTGCTACCAAGACACGATTTTGTGAAGGACATCTTCCACAAGAAACACAGCTGGCT 2270
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 2271 CTCACACTGATAGACACACCGCTCTCGGGCTTCCAGCCCTGCTTCTCCGATGTGAAG 2330
Qy 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 2331 GGCTCCCGCTGTGGGAGAGAGTTCTGAGGATTTGTAGAGCTTCAGAGCCTGACGGCAGCTGTCTGT 2390
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
Db 2391 GCCGGTGGCTGTGCCCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGAGCAGTGT 2450
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 2451 GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGCCCTGGCTGCCCTCCACTTCAACAC 2510
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 2511 AGTGGCATCTGTGAGCTGCACTGCCAGCCCTGCTGCTACCTACAAACAGACACAGCTTTGAG 2570
Qy 281 SerMetProAsnProGluArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
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Qy 361 IleGlnIlePheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 2811 ATCCAGAGATTGTGGCTGCAAGAAGATCTTTGGGAGCCTGGCAATTTCTGCCGGAGAGC 2870
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Db 2871 TTTGATGGGACCCAGGCTCCAAACACTGCCCGCTCCAGCCAGAGCAGCTCCCAAGTGTGT 2930
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 2931 GAGACTCTGGAGAGATCACAGGTTACCTATACATCTCAGCATGGCCGGACAGCTGCCT 2990
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440

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Qy 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
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Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
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Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 3291 TGGGTCCAGGGCCCAACAGTGTGTCACTGCAGCCAGTTCTTCTCGGGCCAGGAGTGC 3350
Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 3351 GTGGAGGAATGCCGAGTACTGCAGGGGCTCCCGCAGGAGTATGTGAATGCCAGGCACTGT 3410
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Qy 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
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Qy 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
Db 3651 GGCTGCCCGCCGAGCAGAGAGAGCCCTCTGACGTCCATCGTCTCTCGGTGGTTGGC 3710
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Db 4731 GACAGACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT 4790
QY 685 GluGluTyrLeuValProGlnGlnGlyPheCysProAspProAlaProGlyAlaGly 704
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RESULT 14
US-09-146-283-3
; Sequence 3, Application US/09146283
; Patent No. 5976546
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
;

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2385 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8
US-09-146-283-3

Alignment Scores:
Pred. No.: 0 Length: 2385
Score: 3632.00 Matches: 659
Percent Similarity: 98.65% Conservative: 0
Best Local Similarity: 98.65% Mismatches: 5
Query Match: 91.86% Indels: 4
DB: 2 Gaps: 2

US-09-493-480-7 (1-712) x US-09-146-283-3 (1-2385)

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QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 131 ACCCACCTGGACATGCTCCGCCACCTCTACACAGGCTGCCAGGCTGGCAGGAAACCTG 190
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspTleGlnGluVal 80
Db 191 GAACTCACCTACTCTGCCACCACCAATGCCAGCTGTCTTCTCTCAGAGATATCCAGGAGGTG 250
QY 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 251 CAGGCTACGTGCTCATCGCTCACCAACCAAGTGGAGGAGTCCCATGTCAGAGGCTGCGG 310
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
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QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuLeuIleGlnArgAsnProGln 160
Db 431 CAGCTTCGAAGCTTCACAGAGATCTTTGAAAGAGGGGTCTTCTATCCAGCGGAACCCCGAG 490
QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 491 CTCTGCTACAGGACACGATTTTGTGGAAGGACATCTTCCACAGAACCAACAGCTGGCT 550

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Db 551 CTCACACTGATAGACACCAACCGCTCTCGGCGCTGCCACCCCTGCTTCTCCGATGTGAAG 610
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Db 671 GCCGGTGGCTGTGCGCCCTGCAAGGGGCCACTGCCCACTGACTGCTGCCATGACGACGTGT 730
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
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Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
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Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
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Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 911 TACAACCTACCTTTCTACGGACGCTGGGATCTGTGACCTGCTGCTGCCCTGCCACCAAC 970
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 971 GAGGTGACAGAGGATGAACACACGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCGA 1030
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Db 1031 GTGTGCTATGCTGGCGCATGGAGCACTTCGGAGAGGTGAGGCGAGTTACAGTGCACAT 1090
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Db 1091 ATCAGGAGTTGTGCTGCTCAAGAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGC 1150
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1151 TTTGATGGGAGCCAGCCTCCAACTGCCCCGCTCCAGCAGAGAGCTCCCAAGTGTGT 1210
Qy 401 GluThrLeuGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 1211 GAGACTCTGGAGAGATCACAGTTACTATACATCTCAGCATGGCGCGAGCCTGCCT 1270
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1271 GACCTCAGCGCTCTCCAGAACCTGCAAGTAAATCCGGGAGCAATTTCTGCACAAATGGCGCC 1330
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1331 TACTCGCTGACCTTGCAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTCCTCAGTGGGAA 1390
Qy 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
Db 1391 CTGGGAGTGGACTGGGCGCTCATCCACCAATAACCCACCTCTGCTTCGTGCACACGGTG 1450
Qy 481 ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
Db 1451 CCCTGGGACCAAGCTCTTTCCGAACCCCGCACCAAGCTCTGCCACACTGCCCAACCGGCCA 1510
Qy 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
Db 1511 GAGGACGAGTGTGGGCGAGGGCGCTGGCTGCCACAGCTGTGCCCGCGAGGCGCACTGC 1570
Qy 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
Db 1571 TGGGTTCCAGGGCCCACTGCTGTCACTGACGACAGTTCTTCTGGGGCCAGGAGTGC 1630

Qy 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
Db 1631 GTGGAGAAATGCCAGTACTGCGAGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1690
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Db 1751 GCTGACCAAGTGTGGCGCTGTGCCCACTATAAGGACCCCTCCCTTCTCGTGGCGCGTGC 1810
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Qy 661 Ala---SerProLeuAspSerThr 667
Db 1982 GCCCGCTGCCCGCAGCCCGCAGCACA 2005

RESULT 15
US-08-579-823A-3
; Sequence 3, Application US/08579823A
; Patent No. 6080409
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Composition and Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,823A
; FILING DATE: 03-DEC-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8

US-08-579-823A-3

Alignment Scores:

Pred. No.:	0	Length:	2385
Score:	3632.00	Matches:	659
Percent Similarity:	98.85%	Conservative:	0
Best Local Similarity:	98.85%	Mismatches:	5
Query Match:	91.86%	Indels:	4
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US-09-493-480-7 (1-712) x US-08-579-823A-3 (1-2385)

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Qy	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
Db	191	GAACCTCACCTACCTGCCACCAATGCCAGCGTGTCTTCTCGAGGATATCCAGGAGGTG	250
Qy	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
Db	251	CAGGGCTACGTGCTCATCGCTCACAACTGAGGAGGAGTCCCTCCCTGAGGATATCCAGGAGGTG	310
Qy	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
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Qy	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
Db	371	GACCCGCTGAACAAATACCAACCCCTGTACAGGGGCTTCCCAGAGGCGCTCGGGAGCTG	430
Qy	141	GlnLeuArgSerLeuThrGluIleLeuIysGlyValLeuIleGlnArgAsnProGln	160
Db	431	CAGCTTCGAAGGCTCACAGAGATCTTGAAGAGAGGGGTCTTGATCAGCGGAAACCCCGAG	490
Qy	161	LeuCysTyrGlnAspThrIleLeuTrpIysAspIlePheHisIysAsnAsnGlnLeuAla	180
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Db	551	CTCACATGATAGACCAACACCGCTCTCGGGCGCTGCCACCCCTGTTCTCCGATGTGTAAG	610
Qy	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220
Db	611	GGCTCCCGCTGTGGGGAGAGATTCTGAGGATTTGTGAGAGCCTGACGGCACTGTCTGT	670
Qy	221	AlaGlyGlyCysAlaArgCysIysGlyProLeuProThrAspCysCysHisGluGlnCys	240
Db	671	GCGGTGGCTGTGCCCGCTGCAGGGGCCACTGCCCACTGACTGCTGCCANGAGAGTGT	730
Qy	241	AlaAlaGlyCysThrGlyProIysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	731	GCTCGCGGCTGCACGGGCCCCAAGCACTCTGACTGCTGCGCTGCCCTTCCACTTCAACCA	790
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Qy	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320

Db 1982 GCCCGCTCGCCGAGCCCCAGCACA 2005

Search completed: August 3, 2005, 13:00:25
Job time : 400.625 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 3, 2005, 12:38:09 ; Search time 1064.29 Seconds
(without alignments)
4329.948 Million cell updates/sec

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Xgapop 10.0, Xgapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3776	95.5	3765	15	US-10-207-498-5 Sequence 5, Appli
2	3776	95.5	3768	9	US-09-811-123-8 Sequence 8, Appli
3	3776	95.5	3768	9	US-09-811-115-2 Sequence 2, Appli
4	3776	95.5	3768	9	US-09-765-973-1 Sequence 1, Appli
5	3776	95.5	3768	9	US-09-854-356-9 Sequence 9, Appli
6	3776	95.5	3768	9	US-09-930-125-1 Sequence 1, Appli
7	3776	95.5	3768	11	US-09-984-092-3 Sequence 3, Appli
8	3776	95.5	3768	16	US-10-313-644-1 Sequence 1, Appli
9	3776	95.5	3768	18	US-10-280-576-3 Sequence 3, Appli
10	3776	95.5	3768	19	US-10-441-779C-3 Sequence 3, Appli
11	3776	95.5	3768	19	US-10-384-339C-52 Sequence 52, Appli
12	3776	95.5	4473	10	US-09-441-411-5 Sequence 5, Appli
13	3776	95.5	4473	15	US-10-146-473-32 Sequence 32, Appli
14	3776	95.5	4473	15	US-10-207-655-44 Sequence 44, Appli
15	3776	95.5	4473	15	US-10-101-510-81 Sequence 81, Appli
16	3776	95.5	4473	20	US-10-762-128-5 Sequence 5, Appli
17	3776	95.5	4473	20	US-10-723-860-8 Sequence 8, Appli
18	3776	95.5	4530	9	US-09-877-177-11 Sequence 11, Appli
19	3776	95.5	4530	15	US-10-177-293-125 Sequence 125, App
20	3776	95.5	4530	15	US-10-007-926A-119 Sequence 119, App
21	3776	95.5	4530	15	US-10-338-730-1 Sequence 1, Appli
22	3776	95.5	4530	15	US-10-101-510-124 Sequence 124, App
23	3776	95.5	4530	17	US-10-116-273-131 Sequence 131, App
24	3776	95.5	4530	17	US-10-426-836-11 Sequence 11, Appli
25	3776	95.5	4530	17	US-10-272-437A-27 Sequence 27, Appli
26	3776	95.5	4530	17	US-10-117-937-595 Sequence 595, App
27	3776	95.5	4530	17	US-10-392-113-45 Sequence 45, Appli
28	3776	95.5	4530	17	US-10-159-563-208 Sequence 208, App
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30	3776	95.5	4530	19	US-10-734-564-59 Sequence 59, Appli
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32	3776	95.5	4530	21	US-10-615-343-16 Sequence 16, Appli
33	3776	95.5	4530	21	US-10-928-465-75 Sequence 75, Appli
34	3776	95.5	4530	21	US-10-794-514A-2 Sequence 2, Appli
35	3776	95.5	4530	21	US-10-871-708-18 Sequence 18, Appli
36	3776	95.5	4530	24	US-11-067-064-595 Sequence 595, App
37	3776	95.5	4642	14	US-10-198-846-10896 Sequence 10896, A
38	3776	95.5	9274	9	US-09-811-123-7 Sequence 7, Appli
39	3776	95.5	9274	9	US-09-811-115-1 Sequence 1, Appli
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42	3733	94.4	4543	9	US-09-769-508-1 Sequence 1, Appli
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45	3595	90.9	2149	17	US-10-412-804A-9 Sequence 9, Appli

ALIGNMENTS

RESULT 1

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; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; TITLE OF INVENTION: METHODS AND MODULATING INTERACTIONS BETWEEN HERGULIN AND HER3
; FILE REFERENCE: 30448.103-US-U1
; CURRENT APPLICATION NUMBER: US/10/207,498
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27

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; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-207-498-5

Alignment Scores:
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Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 15 Gaps: 1

US-09-493-480-7 (1-712) x US-10-207-498-5 (1-3765)

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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
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QY 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGlnGlnCys 240
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RESULT 2
US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-erbB
; TITLE OF INVENTION: ANTIBODY-MAYTANSINOID CONJUGATES
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-811-123-8

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 9 Gaps: 1

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RESULT 3

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US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-115-2
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Alignment Scores:

Pred. No.:	0	Length:	3768
Score:	3776.00	Matches:	712
Percent Similarity:	67.94%	Conservative:	0
Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
DB:	9	Gaps:	1

US-09-493-480-7 (1-712) x US-09-811-115-2 (1-3768)

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QY 141 GlnLeuArgSerLeuThrGluIleLeuValGlyValLeuIleGlnArgAsnProGln 160
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Db	3061	GAGGAGTATCTGGTACCCAGCAGGGCTTCTTCTCTCCAGACCTGCTCCCGGGCGTGGG	3120
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RESULT 4

US-09-765-973-1

; Sequence 1, Application US/09765973

; Publication No. US20020039573A1

; GENERAL INFORMATION:

; APPLICANT: Cheever, Martin A.

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261	Qy	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
781	Db	AGTGGCATCTGTGAGCTGCACTGCCACAGCCCTGGTCACTTACAACACAGACACGTTTGAG	840
281	Qy	SerMetProAsnProGluGlyArgTyrThrPheGlyValaSerCysValThrAlaCysPro	300
841	Db	TCCATGCCCAATCCCGAGGGCCGGTATACATTTGGCGCCAGCTGTGTGACTGCGCTGTGCC	900
301	Qy	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
901	Db	TACAACTACCTTCTACGGACGTGGGATCTTGACCCCTCGTCTGCCCCCTGCACACCAA	960
321	Qy	GluValThrAlaGluAspGlyThrGlnArgCysGluIysCysSerIysProCysAlaArg	340
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341	Qy	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValargAlaValThrSerAlaAsn	360
1021	Db	GTGTGCTATGGTCTGGGCATGGAGCACTTCGAGAGGTGAGGGCAGTTACCACTGGCCAA	1080
361	Qy	IleGlnGluPheAlaGlyCysLysValIlePheGlySerLeuAlaPheLeuProGluSer	380
1081	Db	ATCCAGGAGTTTGTGTGCTGTCAGAGAGTCTTTGGGAGCCTTGGCATTTCTGCCGAGAGC	1140
381	Qy	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
1141	Db	TTTGATGGGACCACAGCCTCCAACTGCCCCGCTCCAGCCAGAGCAGCTCCAAGTGT	1200
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1201	Db	GAGACTCTGGAAGAGATACAGAGTTACCTATACATCTCAGCATGGCCGCGACAGCTGCCT	1260
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1261	Db	GACCTCAGCGCTTCTCAGAACCTTGCAAGTAAATCCGGGACGAATTTGCAACAATGGCGCC	1320
441	Qy	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
1321	Db	TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCCTCCTGAGGGAA	1380
461	Qy	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
1381	Db	CTGGCAGTGGACTGGGCCCTCATCCACATAACACCCACCCTCTGCTCTGTGTCACACGGTG	1440
481	Qy	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
1441	Db	CCCTGGGACCAGCTCTTTGGGAACCCGCAACCAAGCTCTGTCTCACACTGTCGAACCCGCCCA	1500
501	Qy	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
1501	Db	GAGACAGGTGTGTGGCGAGGGCCTGGCCTGCCACCACTGTGTGGCCCCGAGGGCACTGC	1560
521	Qy	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
1561	Db	TGGGCTCCAGGGCCACCAGTGTGTCAACTGTCAGCCAGTTCCTTCTGGGGCCAGGAGTGC	1620
541	Qy	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
1621	Db	GTGGAGGAATGCCCGAGTACTGCAAGGGGCTCCCGAGGGAGTATGTGTAATTCGACGGCACTGT	1680
561	Qy	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
1681	Db	TTGCCGTGCCACCCTGAGTGTTCAGCCCCAGATGGCTCAGTGACCTGTTTGTGACCGGAG	1740
581	Qy	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
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QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
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Db 2521 CTCGTACACAGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAA 2580
QY 653 ----- 653
Db 2581 ATTACAGACTTGGGGTGGCTGGCTGCTGGACATTTAGACAGACAGATPACCATGCAGAT 2640
QY 653 ----- 653
Db 2641 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCGCGCGGGTTACCC 2700
QY 653 ----- 653
Db 2701 CACCAGATGATGTGGAGTTATGTTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
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Db 2761 AAACCTTACGATGGATCCAGCCCGGAGATCCCTGACCTGTGTGAAAAAGGGGAGCGG 2820
QY 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTGTAATGTTGGATG 2880
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QY 653 ----- 653
Db 2881 ATTGACTCTGAATGTGCGCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
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QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACGACACTTCTACCGCTCACTGCTGGAGGACGATGATCGGGGACTGTGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGGTACCCCGACGAGGCTTCTTCTGTCTCAGACCCCTGCCCCGGCGCTGGG 3120
QY 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGGTCCACACGAGCCGCGC 3144

RESULT 5
US-09-854-356-9
; Sequence 9, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
; OTHER INFORMATION: human HER-2/neu protein
; NAME/KEY: misc_feature
; LOCATION: (1)..(1959)
; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (202)..(3765)
; OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (2968)..(3765)
; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (296)..(3144)
; OTHER INFORMATION: preferred portion of the phosphorylation domain
; OTHER INFORMATION: (delta PD) of human HER-2/neu
US-09-854-356-9

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 9 Gaps: 1

US-09-493-480-7 (1-712) x US-09-854-356-9 (1-3768)
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61 GCGAGCACCCAAAGTGTGCACCGGCACAGACATGAAGCTGGGGCTCCCTGTCAGTCCGAG 120
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41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
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61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
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181 GAACCTACCTTACCTGCCCAATATGCCAGCTGTCTTCTGAGGATATCCAGGAGGTG 240
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81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
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241 CAGGGCTACGTGCTCATCGCTCACACCAAGTAGGCAGGTCCCACTGCAGAGGCTGGG 300
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361 GACCCGCTGAACAAATACCACTGTGCACAGGGGCTTCCCAAGAGGCTTGGCGGAGCTG 420
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901 TACAACCTACTTTCTACGAGCGTGGGATCTGTGACCCCTCGTCTGCCCGCTGCACCAACCA 960
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521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
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1561 TGGGTCTCAGGGGCCACCCAGTGTCTCACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC 1620
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1801 CCCAGGGGTGAAACCTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG 1860
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641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
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RESULT 6

US-09-930-125-1
 ; Sequence 1, Application US/09930125
 ; Publication No. US20020193329A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hand-Zimmerman, Susan
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Foy, Teresa M.

; APPLICANT: Lodes, Michael J.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Vedwick, Thomas S.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
 ; FILE REFERENCE: OF HBR-2/NEU-ASSOCIATED MALIGNANCIES
 ; CURRENT APPLICATION NUMBER: US/09/930,125
 ; CURRENT FILING DATE: 2001-08-14
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3768
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(3765)
 US-09-930-125-1

Alignment Scores:
 Pred. No.: 0 Length: 3768
 Score: 3776.00 Matches: 712
 Percent Similarity: 67.94% Conservative: 0
 Best Local Similarity: 67.94% Mismatches: 0
 Query Match: 95.50% Indels: 336
 DB: 9 Gaps: 1

US-09-493-480-7 (1-712) x US-09-930-125-1 (1-3768)

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 Db 121 ACCCACTTGGACATGCTCGCCACCTCTACCAAGGCTGCCAGGTGGTGCAGGGAACCTG 180
 QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
 Db 181 GAACCTCACCTACCTGCCCAACCAATGCCAGCTGTCTCTCTCGAGGATATCCAGGAGTG 240
 QY 81 GlnGlyTyrValLeuIleAlaHisGlnValArgGlnValProLeuGlnArgLeuArg 100
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 QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
 Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTACACATAGA 360
 QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
 Db 361 GACCCGCTGAACAATACACACCCCTGTCAAGGGGCTCCCGAGGAGGCTGCGGGAGCTG 420
 QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
 Db 421 CAGCTTCGAAGCTCACAGAGATCTTGAAGAGAGGGGTCTTGATCCAGCGGAACCCCCAG 480
 QY 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
 Db 481 CTCCTCTACGAGCACCGATTTTGTGGAAGGACATCTTCCACAGAACCAACAGCTGGCT 540
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 QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
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Qy	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
Db	721	GCTGCCGGCTGCAGGGGCCCAAGCACTCTGACTGCTGGCTGGCTGCCCTCCACTTCAACCA	780
Qy	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyraAsnThrAspThrPheGlu	280
Db	781	AGTGGCATCTGTAGCTGCCTGCCCCAGCCCTGGTCACTTACCTACAACACAGACACGTTTGAG	840
Qy	281	SerMetProAsnProGluGlyArgTyThrPheGlyAlaSerCysValThrAlaCysPro	300
Db	841	TCCATGCCCAATCCCGAGGGCGGTATACATTTCGGCGCAGCTGTGTGACTGCTGCTGCC	900
Qy	301	TyrAsnTyLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
Db	901	TACAACATACCTTTCTACGGACGTGGGATCTTCGACACCTCGCTGCCCTCCCTGTCACACACAA	960
Qy	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
Db	961	GAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCAGCAGACCTGTGCCCGA	1020
Qy	341	ValCysTyrglyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
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Qy	361	IleGlnGluPheAlaGlyCysLeuGlyValIlePheGlySerLeuAlaPheLeuProGluSer	380
Db	1081	ATCCAGAGAGTTTGTGCTGTCGAAAGAATCTTTGGAGCCTGGGCATTTCTGCCGGAGAGC	1140
Qy	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
Db	1141	TTTGATGGGGACCCAGCCTCCAAACACTGCCCGCTCCAGCCAGCAGCAGCTCCAAAGTGTTT	1200
Qy	401	GluThrLeuGluGluIleThrGlyTyrglyLeuTyrglySerAlaTrpProAspSerLeuPro	420
Db	1201	GAGACTCTGGAAGAGATCACAGGTTACTATACATCTCAGCATGGCCGGACAGCCTGCGCT	1260
Qy	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
Db	1261	GACCTCAGCGCTTTCCAGAACTTCAAGTATATCCGGGGAGCAATCTTCGCACAATGGCGCC	1320
Qy	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
Db	1321	TACTTCGCTGACCTTGCAAGGCTGGGCATCAGCTGGCTGGGGCTGCGCTCCTCCTGAGGGAA	1380
Qy	461	LeuGlySerGlyLeuAlaLeuIleHisGlnThrHisLeuCysPheValHisThrVal	480
Db	1381	CTGGGCAGTGGACTGGCCCTCATCCACCAATAACACCCACCTCTGCTTCGTGCACACGGTG	1440
Qy	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
Db	1441	CCCTGGGACCAGCTCTTTCCGAAACCCGACCCAGCTCTGTCTCCACACTGCGCAACCGGCCA	1500
Qy	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
Db	1501	GAGACGAGTGTGTGGGCGAGGGCTTGGCTGCCACCCAGCTGTGGCGCCCGAGGGCACTGC	1560
Qy	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
Db	1561	TGGGGTCCAGGGCCCAACCCAGTGTCTCACTGACGACAGTTCTCTTCCGGGGCCAGGAGTGC	1620
Qy	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrrValAsnAlaArgHisCys	560
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Qy	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
Db	1681	TTGCCGTGCCACCCCTGAGTGTGACGCCCAAGTGGCTCAGTGACCTGTTTGTGACGGGAG	1740

QY	581	AlaAspGlnCysValIalaCysAlaHisTyrLysAspProPheCysValIalaArgCys	600
Db	1741	GCTGACCAGTGTGTGGCGTGTGCCCATATAAGAGACCTCCCTTCTTCGCTGGCGCCGCTGC	1800
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
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QY	621	GlyValaCysGlnProCysProIleAenCysThrHisSerCysValaAspLeuAspAspLys	640
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QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
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Qy 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCT 3060
Qy 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGCTACCCAGCAGGCGCTTCTTGTGTCAGACCTTGCCCCCGGCGCTGGG 3120
Qy 705 GlyMetValHisHisArgHisArg 712
Db 3121 GGCATGGTCCACCACAGGCACCGC 3144

RESULT 7
US-09-984-092-3
; Sequence 3, Application US/09984092
; Publication No. US20040037840A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS
; FILE REFERENCE: P1011PC00
; CURRENT APPLICATION NUMBER: US/09/984,092
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
US-09-984-092-3

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 11 Gaps: 1

US-09-493-480-7 (1-712) x US-09-984-092-3 (1-3768)
Qy 1 MetGluLeuAlaAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTGTGCGCGTGGGGCTCTCTCTCGCCCTTGTGCCCGGAGGC 60
Qy 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAAGTGTGCAACCGGCACAGACATGAAGCTCGGGCTCCCTGCCAGTCCCGAG 120
Qy 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu 60
Db 121 ACCACCTGGACATGCTCCGCCACCTCTACCGAGGCTGCCAGTGTGCGAGGAACCTG 180
Qy 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACTCACCTACTGCCCCACCAATGCCAGCTCTCTCTCGAGGATATCCAGGAGGTG 240
Qy 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTACGTGCTCATCGCTCACACCAAGTAGGCGAGGTGCCACTGCGAGGGCTGGCG 300
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Qy 101 lleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGCGCGTGTAGCAATGGA 360
Qy 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAATACCAACCCCTGTCTCAGGGGCTCCCCAGGAGGCTCGCGGAGCTG 420
Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCCAAGCCTCACAGAGATCTTGAAGAGAGGGTCTTGATCCAGCGGAACCCCCAG 480
Qy 161 LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCCTGCTACCAGGACACGATTTTGTGGAGGACATCTTCCACAGAACCAACAGCTGGCT 540
Qy 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAG 600
Qy 201 GlySerArgCysTrpGlySerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCCGCTGCTGGGAGAGAGTTCTGAGGATTGTCTGAGGCTGACGCGCACTGTCTGT 660
Qy 221 AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 661 GCCGCTGGCTGTCGCGCTGCAGGGGCGCACCTGCCCACTGCTGCTGCCATGAGCAGTGT 720
Qy 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGCTGCACGGGCCCCAAGCACCTGACTGCTGCTGCCCTGCCCTCCACTTCAACCCAC 780
Qy 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCACCTGCCCGCCCTGGTGCCTACCAACACACACACGTTTGA 840
Qy 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 841 TCCATGCCCATCCCGAGGGCGGTATACATTCGGGGCCAGCTGTGTGACTGCTGTGCC 900
Qy 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 901 TACAACTACCTTCTACGGACGCTGGGATCCTGCACCCCTGCTGCCCTGCCACCAACCAA 960
Qy 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 961 GAGGTGACAGCAGAGATGGAACACAGCGGTGTGAGAGTGAGCAAGCCCTGTGCGCGGA 1020
Qy 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1021 GTGTGCTATGCTGGGCATGGAGCCTTGCAGAGGTGAGGGCAGTTACCAAGTGCCTAAT 1080
Qy 361 lleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1081 ATCCAGGAGTGTGCTGGCTGCAAGAAGATCTTTGGAGCGCTGGCATTTCTGCGGAGAGC 1140
Qy 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe 400
Db 1141 TTTGATGGGAGCCCCAGCCTCCAACACGCTGCCCTGCCAGCAGAGCAGCTTCCAAGTGT 1200
Qy 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro 420
Db 1201 GAGACTCTGGAAGAGATCACAGTTTACCTATACATCTCAGCATGGCGGACAGCTGCCT 1260
Qy 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla 440
Db 1261 GACCTCAGCGCTCTCCAGAACCTGCAAGTAATCCGGGAGCAAAATCTCGCACAATGCGCC 1320
Qy 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu 460
Db 1321 TACTCGTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGGCTGGCGCTCACTGAGGGAA 1380
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QY 461 LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGCAGTGGACTGGCCCTCATCCACCAATAACACCCACCTTCGCTCGTCACCGGTG 1440
QY 481 ProTirAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCCTGGACACAGCTCTTTTGGAAACCCGACCAAGACTCTGCTCCACACTGCAACCCGGCCA 1500
QY 501 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACGAGTGTGGGCGAGGCGCTGGCCCTGCCACACAGCTGTGGCCGCGAGGCGCACTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGGTCCAGGGGCCACCCAGTGTGTCACTGGACGCGAGTTCCTTCGGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1621 GTGGAGGAATGCCAGTACTGCGAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1681 TTGCCGTGCCACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1740
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys 600
DB 1741 GCTGACCACTGTGGCCTGTGCGCCCACTATAAGAGCCCTCCCTTCGCGTGGCGCGCTGC 1800
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu 620
DB 1801 CCAGCGGTGTGAACCTGACCTCTCTACATCCCATCTGGAAGTTTCCAGATGAGGAG 1860
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLys 640
DB 1861 GGGCGATGCCAGCTTGCCCATCACTGCACCACTCTCTGTGTGGACCTGGATGACAAG 1920
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer 653
DB 1921 GGCTGCCCGCCGAGCAGAGCAGCCCTCTGACGTCCATCTGCTCTGCGGTGGTGGC 1980
QY 653 ----- 653
DB 1981 ATTCTGTGTGTGTGTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040
QY 653 ----- 653
DB 2041 AAGATCCGGAAGTACAGATGCGGAGACTGCTGCAGAAACGGAGCTGTGGTGGAGCCGCTG 2100
QY 653 ----- 653
DB 2101 ACACCTAGCGAGCGATGCCAACACGAGCGCAGATCGGATCCTGAAAGAGAGCGAGCTG 2160
QY 653 ----- 653
DB 2161 AGGAAGTGAAGTGTGTGATCTGGCGTTTGGCACAGTCTACAAGGGCATCTGGATC 2220
QY 653 ----- 653
DB 2221 CCTGATGGGGAATGTGAAATTCAGTGGCCCATCAAGTGTGAGGGAACACATCC 2280
QY 653 ----- 653
DB 2281 CCCAAAGCCAAAGAAATCTTAGAGAGAGCATACTGTGATGCTGTGTGGGCTCCCCA 2340
QY 653 ----- 653
DB 2341 TATGTCTCCGCCTTCTGGGCACTCTGCCCTGACATCCACGGTGCAGTGTGTGACACAGCTT 2400
QY 653 ----- 653
DB 2401 ATGCCCTATGGCTCTTAGACCATGTCCGGGAAACCGCGGACGCTGGGCTCCCG 2460
QY 653 ----- 653

DB 2461 GACCTGCTGAACCTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTCCGG 2520
QY 653 ----- 653
DB 2521 CTCGTACACAGGGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAAA 2580
QY 653 ----- 653
DB 2581 ATTACAGACTTGGGGTGGCTGGCTGGCTGGACATTGACAGACAGATACCATGCAGAT 2640
QY 653 ----- 653
DB 2641 GGGGGCAAGGTGCCCATCAAGTGGATGGGCTGGAGTCCATTCTCCGCGCGCGGTTCCAC 2700
QY 653 ----- 653
DB 2701 CACCAGAGTATGTGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
QY 653 ----- 653
DB 2761 AAACCTTACGATGGGATCCAGCCCGGAGATCCCTGACCTGCTGGAAAAGGGGAGCGG 2820
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DB 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGTCAAATGTTGGATG 2880
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DB 2881 ATTGACTCTGAATGTGCGCCAGATTCGGGAGTTGGTGTCTGAATTCCTCCGATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
DB 2941 AGGGACCCCGAGCGCTTGTGTGTCATCCAGAAATGAGGACTTGGGCGCAGCCAGTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetClyAspLeuValAspAla 684
DB 3001 GACAGCACCTTCTACCGCTCCTGCTGGAGGAGGATGACATGGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3061 GAGGAGTATCTGTACCCCGCAGCAGGCGCTTCTGTCTCAGACCTGCCCCGGCGCTGGG 3120
QY 705 GlyMetValHisHisArgHisArg 712
DB 3121 GGCATGGTCCACACACAGGACCGC 3144

RESULT 8

US-10-313-644-1
; Sequence 1, Application US/10313644
; Publication No. US20030157119A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmerman, Susan
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; FILE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.483C3
; CURRENT APPLICATION NUMBER: US/10/313,644
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-313-644-1

Alignment Scores:

Pred. No.: 0 Length: 3768

Score:	3776.00	Matches:	712
Percent Similarity:	67.94%	Conservative:	0
Best Local Similarity:	67.94%	Mismatches:	0
Query Match:	95.50%	Indels:	336
DB:	16	Gaps:	1
US-09-493-480-7 (1-712) x US-10-313-644-1 (1-3768)			
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DB	1	ATGGAGCTGGCGCCTTGTGGCGCTGGGGCTCCTCTCGCCCTCTTGGCCCCCGGAGCC	60
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu	40
DB	61	GGGAGCACCAAGTGTGCACCGGCACAGACATGAAGTCGGGCTCCTCCAGTCCCGAG	120
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlyAsnLeu	60
DB	121	ACCCACCTGGACATGCTCCGCCACCTCTACCAAGGCTGCAGGTGGTCAGGGAACCTG	180
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
DB	181	GAACTCACCTACTGCGCCACCAATGCCAGCTGTCTCTCGAGGATATCCAGAGGTG	240
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
DB	241	CAGGGCTAGCTGCATCGCTCACACCAAGTGAGGCAGGTCCCACTGCAGAGGCTGGG	300
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
DB	301	ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCTGGCCGTGTAGACAAATGA	360
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
DB	361	GACCCCTGAACAATACCAACCTGTGCAGGGGCTCCCGAGGAGCTGGGGAGCTG	420
QY	141	GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln	160
DB	421	CAGCTTCGAAGCTCACACAGATCTTTGAAGGAGGGGTCTTGATCCAGCGGAACCC	480
QY	161	LeuCysTyrGlnAspThrIleLeuTrpLysAspIlePheHisLysAsnGlnLeuAla	180
DB	481	CTCTGCTACAGGACACGATTTTGTGAAGGACATCTTCCACAAGAACCAACAGCTGG	540
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	541	CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCTCTTCTCCGATGTGTAG	600
QY	201	GlySerArgCysTrpGlyGluSerGluAspCysGlnSerLeuThrArgThrValCys	220
DB	601	GGCTCCCGCTGTGGGGAGAGATTCTGAGGATTTGTACAGGCTGCAGCGCACTGTCTGT	660
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysHisGlnGlnCys	240
DB	661	GGCGGTGGCTGTGCCGCTGCAGGGGCCACTGCCCACTGACTGTGTCCTCAGCAGTGT	720
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	721	GCTGCCGGCTGCAGGGGCCCAAGCACTCTGACTGCTTGGCTGGCTGCCCTTCAACAC	780
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
DB	781	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGGTCACCTACAAACACACACACGTTT	840
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
DB	841	TCCATGCCCAATCCCGAGGGCGGTATACATTCGGCGCCAGCTGTGTGACTGCCTGCC	900
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	901	TACAACTACTTTTACGAGAGCTGGGATCTGCACCTCTGTGCCCTCCCTGCACAAACCA	960
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340

DB	961	GAGGTGACAGAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGAAAGCCCTGTGCCGA	1020
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1021	GTGTGCTATGGTCTGGGCATGGAGCATTGGAGAGGTGAGGGCAGTTACCACTGCAAT	1080
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1081	ATCCAGGAGTTTGTGGCTGCAAGAAGATCTTTGGAGGCTGGCATTTCTGCCGAGAGC	1140
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
DB	1141	TTTGTATGGGACCCAGCTCCAAACACTGCCCGCTCCAGCCAGCAGCTCCCAAGTGT	1200
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
DB	1201	GAGACTCTGGAAGAGATCACAGGTACCTATACATCTCAGCATGGCCGACAGCTGCCT	1260
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	1261	GACCTCAGGCTCTTCAGAACCTGCAGTAAATCCGGGACGAAATTCGCACANTGGGCG	1320
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1321	TACTCGCTGACCTGCAAGGGCTGGGCATCAGTGGCTGGGCTGGCTCACTGAGGAA	1380
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
DB	1381	CTGGCAGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTGTGTGCACAG	1440
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	1441	CCCTGGGACCACTCTTTGGNAACCCGACCCAGCTCTGCTCCACACTGCCAACCGGCA	1500
QY	501	GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	1501	GAGGACGAGTGTGGGGAGGGCTGGCTGCCACCACTGCTGGCCCGCCAGGGCACTGC	1560
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	1561	TGGGTCCAGGGCCCAACCCAGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTG	1620
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
DB	1621	GTGGAGGAAATGCCGAGTACTGCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACT	1680
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	1681	TTGCCGTGCCACCTGTAGTGTGAGCCCAAGATGGCTCAGTGCACCTGTTTGGACCGGAG	1740
QY	581	AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys	600
DB	1741	GCTGACCACTGTGTGGCTGTGCCACATATAGGACCTTCCCTCTGCGTGGCCGCTGC	1800
QY	601	ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPheProAspGluGlu	620
DB	1801	CCCAGCGTGTGAACCTTGACCTCTCTACATGCCCATCTGGAAGTTTCCAGATGAGGAG	1860
QY	621	GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspLeuLys	640
DB	1861	GGCGCATGCCAGCTTGGCCCATCACTCACTGCACCCACTCTGTGTGGACCTGTGATGACA	1920
QY	641	GlyCysProAlaGluGlnArgAlaSerProLeuThrSer	653
DB	1921	GGCTCCCCCGGAGAGAGAGCCCTCTGACGTCCATCATCTCTGCGGTGTGTGGC	1980
QY	653	-----	653
DB	1981	ATTCTGCTGGTGTGTGGGGTGTCTTTGGGATCCTCATCAAGCAGCGGAGCAG	2040
QY	653	-----	653

Db 2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGGAAACGGAGCTGGTGGAGCCGCTG 2100
QY 653 ----- 653
Db 2101 ACACCTAGCGAGCGATGCCAACACGAGCGAGATCGGATCCTGAAAGAGACGGAGCTG 2160
QY 653 ----- 653
Db 2161 AGAAGGTGAAGTGTGGATCTGGCGCTTTTGGCACAGTCTACAAGGCGATCTGGATC 2220
QY 653 ----- 653
Db 2221 CCTGATGGGAGATGTGAAAATTCAGTGGCCATCAAAGTGTGAGGGAAAAACACATCC 2280
QY 653 ----- 653
Db 2281 CCCAAAGCCAAACAAAGAAATCTTAGACGAAGCATACGTGATGGTGTGGGTCCCCA 2340
QY 653 ----- 653
Db 2341 TATGTCTCCGCTTCTGGGCATCTGCTGACATCCACGGTGCAGCTGGTGACACAGCTT 2400
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Db 2401 ATGCCCTATGGCTGCTCTTAGACCATGTCCGGGAAACCGCGAGCGCTGGGCTCCAG 2460
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Db 2461 GACCTGCTGAATGGTGTATGCAGATTGCCAAGGGATGAGTACCTGGAGGATGTGCGG 2520
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Db 2521 CTCGTACACAGGACTTGGCGCTCGGAACGTGTGTCAGAGTCCCAACCATGTCAAA 2580
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Db 2581 ATTACAGACTTCGGGCTGGCTCGGCTGTGACATTTGACAGACAGATACCATGCAGAT 2640
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Db 2641 GGGGGCAAGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGTTCAAC 2700
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Db 2701 CACCAGAGTGATGTGGAGTTATGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
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Db 2761 AAACCTTACGATGGATCCAGCGCCGGGAGATCCCTGACCTGTGGAAGGGGGAGCGG 2820
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Db 2821 CTGCCCCAGCCCCCATCTGCACCATTTGATGTCTACATGATCATGGTCAAAATGTGGATG 2880
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Db 2881 ATTGACTCTGAATGTCCGCCAAGATTCCGGGAGTTGGTGTCTGAATTTCTCCCGCATGGCC 2940
QY 654 ----- GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGAGCCCCAGCGCTTTGTGGTATCTCAGAAATGAGGACTTGGGCCCGAGCCAGTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGACCTTCTACCGCTCACTGTGGAGGACGATGACATGGGGNACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGGTACCCAGCAGGGCTTCTTCTGTCCAGACCTTGCCCCGGGCGCTGGG 3120
QY 705 GlyMetValHisArgHisArg 712
Db 3121 GGCATGTGTCACCACAGGCCCGC 3144

RESULT 9

US-10-280-576-3
; Sequence 3, Application US/10280576
; Publication No. US20040044405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280,576
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-280-576-3

Alignment Scores:

Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 18 Gaps: 1

US-09-493-480-7 (1-712) x US-10-280-576-3 (1-3768)

QY 1 MetGluLeuAlaAlaLeuCysArgTyrGlyLeuLeuLeuAlaLeuProProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTGTGCGCTGGGGCTCTCTCTCGCCCTTGTCCCGAGCC 60
QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGACCCAAAGTGTGCACCGGCACAGACATGAAGCTGCGGCTCCCTGCCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnValAsnLeu 60
Db 121 ACCACCTGGACATGTCTCGCCACCTCTACCGAGGCTGCCAGGTGTGTCAGGGNAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACTCACCTACCTGCCCAATGCGAGCTGTCTCTCTGTCAGGATATCCAGGAGGTG 240
QY 81 GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGCTCATCGCTCAACCAAGTGAAGCAGGTCCCTGTCAGAGGCTGCGG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACATATGCTGCGCCCTGTCTAGACATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACAATACCACTGTCACAGGGGCTCCCGCAGGAGGCTGCGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCCTCAAGAGATCTTGAAGGAGGGGTCTTGATCAGCGGAAACCCCGAG 480
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnGlnLeuAla 180
Db 481 CTCCTGTACAGGACACGATTTTGTGGAAGGACATCTTCCACAAAGAACCAACAGCTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCGCTCTCGGGCTGCCACCCCTGTTCTCCGATGTGTAAAG 600
QY 201 GlySerArgCysTyrGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220


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QY 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCAATTGATGTCTACATGATCATGTGTCAAATGTTGGATG 2880
QY 653 ----- 653
Db 2881 ATTGACTCTGAATGTGCGGCCAAGATTCGCGAGTGTGTGTGTAATTCTCCCGCATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGAGCCCCAGCGCTTTGTGGTCATCCAGAAATGAGGACTTGGCCCCAGCCAGTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGAGTATCTGTACCCGAGCAGGGCTTCTTCTGTCCAGACCTGCCCCGGGGCTGGG 3120
QY 705 GlyMetValHisArgHisArg 712
Db 3121 GGCATGGTCCACCACAGGCCCGC 3144

RESULT 10
US-10-441-779C-3
; Sequence 3, Application US/10441779C
; Publication No. US20040141958A1
; GENERAL INFORMATION:
; APPLICANT: Steinaa, Lucilla
; APPLICANT: Mouritsen, Soren
; APPLICANT: Gautam, Anand
; APPLICANT: Haaning, Jesper
; APPLICANT: Dalum, Iben
; APPLICANT: Birk, Peter
; APPLICANT: Leach, Dana
; APPLICANT: Nielsen, Klaus
; APPLICANT: Karlsson, Gunilla
; TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
; FILE REFERENCE: 4614-0116P
; CURRENT APPLICATION NUMBER: US/10/441,779C
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 09/413,186
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/105,011
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: PA 1998 01261
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3768)
; OTHER INFORMATION:
US-10-441-779C-3

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 19 Gaps: 1

US-09-493-480-7 (1-712) x US-10-441-779C-3 (1-3768)

QY 1 MetGluLeuAlaAlaLeuCysArgTTPGlyLeuLeuLeuAlaLeuLeuProProGlyAla 20
Db 1 ATGGAGCTGGCGGCTTGTGCCCGCTGGGGGCTCTCTCTCGCCCTCTTGGCCCGGAGGC 60
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QY 21 AlaSerThrGlnValCysThrGlyThrAspMetLysLeuArgLeuProAlaSerProGlu 40
Db 61 GCGAGCACCAAGTGTGCACCGGCACAGACATGAAGCTGGGGTCTCCCTGCGCAGTCCCGAG 120
QY 41 ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnValAsnLeu 60
Db 121 ACCCACTGGACATGTCTCGCCACCTCTACCAAGGCTGCCAGGTGGTGGAGGAAACCTG 180
QY 61 GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal 80
Db 181 GAACTCACCTACTGCTGCCACCAATGCGAGCTGTCTCTCTGAGGATATCCAGGAGGTG 240
QY 81 GlnGlyTyrValLeuLeuAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg 100
Db 241 CAGGGCTAGCTGTCTCATCGCTCAACAACCAAGTGAGGAGGCTCCCACTGCAGAGGCTCGG 300
QY 101 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly 120
Db 301 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACTATGCCCCCTGGCCGTGTAGACAATGGA 360
QY 121 AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu 140
Db 361 GACCCGCTGAACATACCACTACCCCTGTCAACAGGGGCTCCCAAGAGGCTGCGGGAGCTG 420
QY 141 GlnLeuArgSerLeuThrGluLeuLeuLysGlyValLeuLeuGlnArgAsnProGln 160
Db 421 CAGCTTCGAAGCTCACAGAGATCTTTGAAGGAGGGGTCTTGATCCAGCGGAACCCCGAG 480
QY 161 LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla 180
Db 481 CTCCTGTACAGGACACGATTTTGTGGAAGGACATCTTCACAGAACAACACCACTGGCT 540
QY 181 LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys 200
Db 541 CTCACACTGATAGACACCAACCCCTCTCGGGCTGCAACCCCTGTCTCCGATGTGTAG 600
QY 201 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys 220
Db 601 GGCTCCGCTGTCTGGGAGAGATCTGAGGATTTGTAGAGCTGTGAGAGCTGCGCGCACTGT 660
QY 221 AlaGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys 240
Db 661 GCGGTGGCTGTGCGCGCTGCAAGGGGCCACTGCCCACTGCTGCTGCTGCTGCTGCTGCTG 720
QY 241 AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis 260
Db 721 GCTGCCGGCTGCACGGGCCCCCAAGCACTCTGACTGCTGCGCTGCTGCTGCTGCTGCTG 780
QY 261 SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu 280
Db 781 AGTGGCATCTGTGAGCTGCCTGCCAGCCCTGGTCACTTACCAACACAGACAGCTTTGAG 840
QY 281 SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro 300
Db 841 TCCATGCCCAATCCCGAGGGCGGTATACATTCGGGCGCCAGCTGTGTGACTGCTGCTGCC 900
QY 301 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln 320
Db 901 TACAACTACTTCTACGGACGTGGGATCTCTGCACCCCTGTCTGCCCCCTGCAACACCAA 960
QY 321 GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg 340
Db 961 GAGGTGACAGCAGAGGATGGACACACAGCGGTGTGAGAAGTGCAGCAAGCCCTGTGCCCCGA 1020
QY 341 ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn 360
Db 1021 GTGTGCTATGGTCTGGGCATGGAGCACTTGCAGAGGTGAGGCGATGTACCACTGCGCAAT 1080
QY 361 IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer 380
Db 1081 ATCCAGGATTTGCTGGCTGCAAGAGATCTTTGGAGGCTGCGCATTTCTGCCCGGAGGC 1140
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QY 381 PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuValPhe 400
DB 1141 TTTGATGGGAGCCAGCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT 1200
QY 401 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTyrProAspSerLeuPro 420
DB 1201 GAGACTCTGGAAGAGATCACAGGTTACCTATATACATCTCAGCATGGCGGACAGCCTGCCT 1260
QY 421 AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisGlnAla 440
DB 1261 GACCTCAGCGTCTTCAGAACCTTCCAGAGTAATCCGGGGAGCAATCTGCACAAATGGCGCC 1320
QY 441 TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTyrLeuGlyLeuArgSerLeuArgGlu 460
DB 1321 TACTCGCTGACCTGCAAGGGCTGGGCATCAGCTGGCTGGGCTGGCTCACTGAGGGAA 1380
QY 461 LeuGlySerGlyLeuAlaLeuIleHisHisAsnThrHisLeuCysPheValHisThrVal 480
DB 1381 CTGGGCAGTGGACTGGCCCTCATCCACCATAACACCCACCTCTGCTTCGTGCACACGGTG 1440
QY 481 ProTyrAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro 500
DB 1441 CCTGGGACACAGCTCTTTCCGAAACCCGACCAAGCTCTGCTCCACACTGCCAACCGGCCA 1500
QY 501 GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys 520
DB 1501 GAGGACAGTGTGTGGCGCAGGGCTGGCTGCCACCACTGTGCCCGCGAGGGCACTGC 1560
QY 521 TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys 540
DB 1561 TGGGGTCCAGGGCCACCCAGTGTGTCAACTGCAGCCAGTTCCTTCGGGGCCAGGAGTGC 1620
QY 541 ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys 560
DB 1621 GTGGAGGAATCCGAGTACTGACAGGGGCTCCCGAGGAGTATGTGAATCCAGGCACGTGT 1680
QY 561 LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu 580
DB 1681 TTGGCGTGCACCCCTGAGTGTGAGCCCCCAGAGATGGCTCAGTGACCTGTTTTGGACGGAG 1740
QY 581 AlaAspGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
DB 1741 GCTGACCACTGTGTGGCCTGTGCCACTATAAGGACCCCTCCCTTCTGCGTGGCCCGCTGC 1800
QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
DB 1801 CCAGCGGTGTGAACCTGACCTCTCTACATGCCCATCTGGAAGTTTTCCAGATGAGGAG 1860
QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
DB 1861 GGGCATGCCAGCCTTGCCCCCATCAACTGCACCCCACTCTGTGTGGACCTGGATGACAA 1920
QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer- 653
DB 1921 GGTGTCGCCCGCGAGCAGAGCCAGCCCTCTGACGTCCATCGTCTCTCGCGTGGTTGGC 1980
QY 653 ----- 653
DB 1981 ATTCTGCTGGTCTGTGGGGTGGTCTTTGGGATCCTCATCAAGCGACGGAGCGAG 2040
QY 653 ----- 653
DB 2041 AAGATCCGGAAGTACACGATGCGGAGACTGCTGCAGAAACGGAGTGGTGGAGCGCGTG 2100
QY 653 ----- 653
DB 2101 ACACCTAGCGGAGCGATGCCAACACGAGCGCAGATGCCGATCCTGAAAGACGGAGCTG 2160
QY 653 ----- 653
DB 2161 AGGAAGTGAAGTGTGGATCTGGCGCTTTGGCACAGTCTACAGGGCATCTGGATC 2220
QY 653 ----- 653

DB 2221 CCTGATGGGAGAGTGTGAAAATTCCAGTGGCCATCAAAGTGTTCGAGGAAAACACATCC 2280
QY 653 ----- 653
DB 2281 CCCAAAGCCAAAGAAAATCTTAGACGAAGCATACGTGATGGTGGTGGTGGCTCCCA 2340
QY 653 ----- 653
DB 2341 TATGTCTCCGCCTTCTGGGCATCTGGCATCTGCCTGACATCCACGGTGCAGCTGGTGCACAGCTT 2400
QY 653 ----- 653
DB 2401 ATGCCCTATGCTGCTCTTTAGACCATGTTCGGGAAAACCGCGGACGCTGGGCTCCAG 2460
QY 653 ----- 653
DB 2461 GACCTGCTGAACGTGGTGTATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGCG 2520
QY 653 ----- 653
DB 2521 CTCGTACACAGGGACTTGGCCGCTCGGAACGTGTGTTCAAGAGTCCCACCATGTCAAA 2580
QY 653 ----- 653
DB 2581 ATTACAGACTTCGGGCTGGCTGGCTGTGGACATTGACGAGACAGAGTACCATGCAGAT 2640
QY 653 ----- 653
DB 2641 GGGGCAAGGTGCCCATCAAGTGGATGGCGTGGAGTCCATTCTCCGCGCGGTTCAAC 2700
QY 653 ----- 653
DB 2701 CACCAGAGTATGTGTGGAGTTATGTTGTTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760
QY 653 ----- 653
DB 2761 AAACCTTAGATGGATCCAGCCCGGAGATCCCTGACCTGCTGMAAAGGGGAGCGG 2820
QY 653 ----- 653
DB 2821 CTGCCCCAGCCCCCATCTGCACCATTGTATGATGCTATCATGATCATGTTCAATGTTGGATG 2880
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DB 2881 ATTGACTCTGATGTGCGGCAAGATTCGGGAGTTGGTGTCTGAATTCTCCCGCATGGCC 2940
QY 654 -----GlnAsnGluAspLeuGlyProAlaSerProLeu 664
DB 2941 AGGACCCCGCAGCGCTTTGTGTGTCATCCAGAATGAGGACTTGGGCCAGCCAGTCCCTTG 3000
QY 665 AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAspLeuValAspAla 684
DB 3001 GACAGACCTTCTACCGCTCACTGCTGGAGGACGATGATGCGGGACCTGGTGGATGCT 3060
QY 685 GluGluTyrLeuValProGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
DB 3061 GAGGAGTATCTGTTACCCCGACAGCGGCTTCTCTGTCCAGACCTTGCCCGGCGCTGG 3120
QY 705 GlyMetValHisHisArgHisArg 712
DB 3121 GGCATGGTCCACCACAGCACCGC 3144

RESULT 11

US-10-384-339C-52
; Sequence 52, Application US/10384339C
; Publication No. US20040175703A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Roland
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GEN
; FILE REFERENCE: 20200/2002
; CURRENT APPLICATION NUMBER: US/10/384,339C
; CURRENT FILING DATE: 2003-03-07

; PRIOR APPLICATION NUMBER: PCT/EP02/00152
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: DE 10100586.5
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: DE 10155280.7
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: DE 10158411.3
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: DE 10160151.4
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; TITLE: ERBB2
; PATENT DOCUMENT NUMBER: NM004448
; US-10-384-339C-52

Alignment Scores:
Pred. No.: 0 Length: 3768
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 19 Gaps: 1

US-09-493-480-7 (1-712) X US-10-384-339C-52 (1-3768)

QY	1	MetGluLeuAlaLeuCysArgTTPGlyLeuLeuAlaLeuProProGlyAla	20
DB	1	ATGGAGCTGGCGGCTTGTGCGCTGGGGCTCTCTCGCCCTCTTGGCCCGGAGCC	60
QY	21	AlaSerThrGlnValCysThrGlyThrAspMetTlyLeuArgLeuProAlaSerProGlu	40
DB	61	GCAGAGCAACCAAGTGTGCACCGGCACAGATGAAGCTGGGGCTCCCTGCCAGTCCCGAG	120
QY	41	ThrHisLeuAspMetLeuArgHisLeuTyrGlnGlyCysGlnValValGlnGlnValAsnLeu	60
DB	121	ACCCACTGACATGCTCCCGCCACTCTACAGGGCTGCCAGGTGGTGCAGGGNAACCTG	180
QY	61	GluLeuThrTyrLeuProThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluVal	80
DB	181	GAACCTACCTACCTGCCCAATGCCAGCTGTCTCTCTGTCAGGATATCCAGGAGGTG	240
QY	81	GlnGlyTyrValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg	100
DB	241	CAGGGCTACGTGTCTATCGCTCAACCAAGTGAAGGAGGCTCCCACTGCAGAGGCTGCGG	300
QY	101	IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaValLeuAspAsnGly	120
DB	301	ATTGTGCGAGCACCCAGCTCTTTGAGGACAACTATGCCCCCTGGCGTGTAGACAAATGA	360
QY	121	AspProLeuAsnAsnThrThrProValThrGlyAlaSerProGlyGlyLeuArgGluLeu	140
DB	361	GACCCGTGAACAATACCAACCCCTGTCAAGGGGCTCCCGAGAGGCTCGCGGAGCTG	420
QY	141	GlnLeuArgSerLeuThrGluIleLeuLeuGlyGlyValLeuIleGlnArgAsnProGln	160
DB	421	CAGCTTCGAAGCTCACAGAGATCTTGAAGAGGGGTCTTGATCCAGCGGNAACCCCGAG	480
QY	161	LeuCysTyrGlnAspThrIleLeuTyrLysAspIlePheHisLysAsnAsnGlnLeuAla	180
DB	481	CTCTGCTACCAAGACATGTTTGTGGAGGACATCTTCCCAAGAACCAACCAAGTGGCT	540
QY	181	LeuThrLeuIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys	200
DB	541	CTCACATGATAGACCAACCGCTCTCGGGCTGCGCCCTGTCACCCCTGTTCTCCGATGTGTAAG	600
QY	201	GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuThrArgThrValCys	220

DB	601	GGCTCCCGCTGCTGGGAGAGAGATTCTGAGGATTGTGAGAGCTGAGCGCACTGTCTGT	660
QY	221	AlaGlyGlyCysAlaArgCysLysGlyProLeuProThrAspCysCysHisGluGlnCys	240
DB	661	GCCGGTGGCTGTGCCCCGCTGCAAGAGGGCCACTGCCCACTGACTGCTGCATGAGCAGTGT	720
QY	241	AlaAlaGlyCysThrGlyProLysHisSerAspCysLeuAlaCysLeuHisPheAsnHis	260
DB	721	GCTGCCGGCTGCACGGGCCCAAGCACTCTGACTGCTGGCCTGCCCTTCACTTCAACAC	780
QY	261	SerGlyIleCysGluLeuHisCysProAlaLeuValThrTyrAsnThrAspThrPheGlu	280
DB	781	AGTGGCATCTGTGAGCTGCACCTGCCAGCCCTGCTCACCTACACACACAGACAGTTTGA	840
QY	281	SerMetProAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro	300
DB	841	TCCATGCCCAATCCCGAGGGCGGTATACATTCGGCGCCAGCTGTGTGACTGCTGCTCCC	900
QY	301	TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysProLeuHisAsnGln	320
DB	901	TACAACCTACCTTTCTACGGACGTGGGATCCTGCAACCTCTGCTGCCCTTGCACACCA	960
QY	321	GluValThrAlaGluAspGlyThrGlnArgCysGluLysCysSerLysProCysAlaArg	340
DB	961	GAGTGACAGCAGAGAGATGGACACAGCGGTGTGAGAGTGCAGAGAGCCCTGTGCCCGA	1020
QY	341	ValCysTyrGlyLeuGlyMetGluHisLeuArgGluValArgAlaValThrSerAlaAsn	360
DB	1021	GTGTGCTATGCTGGGCATGGAGCACTTGCAGAGAGTGGAGGAGTTACAGTGCCTCAAT	1080
QY	361	IleGlnGluPheAlaGlyCysLysLysIlePheGlySerLeuAlaPheLeuProGluSer	380
DB	1081	ATCCAGAGGTTTGTGCTGCTGCAAGAGATCTTTGGGAGCCTGGCATTTCTGCCGGAGAGC	1140
QY	381	PheAspGlyAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe	400
DB	1141	TTTGTATGGGAGACCCAGCCTCCAACTGCCCTCCAGCCAGAGAGAGCTCCAAAGTGT	1200
QY	401	GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpProAspSerLeuPro	420
DB	1201	GAGACTCTGGAAGAGATCAAGGTTACCTATATACATCTCAGCATGGCGGAGAGCTGCCT	1260
QY	421	AspLeuSerValPheGlnAsnLeuGlnValIleArgGlyArgIleLeuHisAsnGlyAla	440
DB	1261	GACCTCAGCGCTCTTCCAGAACCTGCAAGTAATCCGGGAGCAATTTCTGCAAAATGGCGCC	1320
QY	441	TyrSerLeuThrLeuGlnGlyLeuGlyIleSerTrpLeuGlyLeuArgSerLeuArgGlu	460
DB	1321	TACTGCTGACCTGCAGGGCTGGGCATCAGCTGGCTGGGGCTGGCTCCTCCTCCTGAGGAA	1380
QY	461	LeuGlySerGlyLeuAlaLeuIleHisAsnThrHisLeuCysPheValHisThrVal	480
DB	1381	CTGGGAGTGGACTGGCCCTCATCCACCAATAACACCCACTCTGCTTCGTGCACACGGTG	1440
QY	481	ProTrpAspGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro	500
DB	1441	CCCTGGGAGCAGCTCTTTCCGAAACCCGCACTGCTGCTCCACTGCACTGCCAACCCGCCA	1500
QY	501	GluAspGluCysValGlyGlyLeuAlaCysHisGlnLeuCysAlaArgGlyHisCys	520
DB	1501	GAGACAGATGTGTGGCGGAGGCTGGCCCTGCCACAGCTGCGCGCCGAGGCACTGC	1560
QY	521	TrpGlyProGlyProThrGlnCysValAsnCysSerGlnPheLeuArgGlyGlnGluCys	540
DB	1561	TGGGGTCCAGGGCCCACTGCTGTCACTGACAGCAGTTCTCTTGGGGCCAGGAGTGC	1620
QY	541	ValGluGluCysArgValLeuGlnGlyLeuProArgGluTyrValAsnAlaArgHisCys	560
DB	1621	GTGGAGGAAATGCCAGTACTGTCAGGGGCTCCCGAGGAGTATGTGAATGCCAGGCACTGT	1680
QY	561	LeuProCysHisProGluCysGlnProGlnAsnGlySerValThrCysPheGlyProGlu	580
DB	1681	TTGCCGTGCCACCTCAGTGTGTCAGCCCAAGATGGCTCAGTACCTGCTTTTGGACCCGAG	1740

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QY 581 AlaAepGlnCysValAlaCysAlaHisTyrLysAspProPheCysValAlaArgCys 600
Db 1741 GTGACCAAGTGTGGCCCTGTGCCCACTATAGGACCTCCCTTCTGCGTGGCCCGCTGC 1800

QY 601 ProSerGlyValLysProAspLeuSerTyrMetProIleTyrLysPheProAspGluGlu 620
Db 1801 CCCAGCGGTGTGAACCTGACCTCTCTACATGCTCCATCTGGAAGTTTCCAGATGAGGAG 1860

QY 621 GlyAlaCysGlnProCysProIleAsnCysThrHisSerCysValAspLeuAspAspLys 640
Db 1861 GCGCATGCGACGCTTGCCCACTCAACTGCACCCACTCCTGTGTGAGCACTGGATGACAA 1920

QY 641 GlyCysProAlaGluGlnArgAlaSerProLeuThrSer----- 653
Db 1921 GGCTGCCCCCGCAGCAGCAGAGCAGCCCTCTGACGTCCATCGTCTCTCGGTGGTTGGC 1980

QY 653 ----- 653
Db 1981 ATTCTGCTGGTGTCTTGGGGTGGTCTTTTGGGATCCTCATCAAGCGACGGCAGCAG 2040

QY 653 ----- 653
Db 2041 AAGATCCGGAAGTACACGATGCGGAGCTGCTCAGGAAACGGAGCTGGTGGAGCGCTG 2100

QY 653 ----- 653
Db 2101 ACACCTAGCGGAGCGATGCCAACCGCGCAGATGCGGATCCTGNAAGACGAGCTG 2160

QY 653 ----- 653
Db 2161 AGGAAGGTGAAGTGTCTGGATCTGGCGCTTTTGGCACAGTCTACAAGGGCATCTGGATC 2220

QY 653 ----- 653
Db 2221 CTTGATGGGGAGATGTGAAATTCAGTGGCCATCAAAAGTGTGAGGAAACACATCC 2280

QY 653 ----- 653
Db 2281 CCCAAAGCCAAACAGAAATCTTAGACGAAGCATAGTGTGGTGGTGGCTCCCA 2340

QY 653 ----- 653
Db 2341 TATGTCTCCGCTTCTGGGCATCTGCCTGCATCCACGGTGCAGCTGGTGCACAGCTT 2400

QY 653 ----- 653
Db 2401 ATGCCCTATGGTGCTCTTTAGACCATGTCCGGGAAACCGCGAGCGCTGGGCTCCAG 2460

QY 653 ----- 653
Db 2461 GACCTGCTGAACCTGGTGATGCAGATTGCCAAGGGGATGAGCTACCTGGAGGATGTGG 2520

QY 653 ----- 653
Db 2521 CTGATACACAGGACTTGGCCGCTCGGAACGTGCTGGTCAAGAGTCCCAACCATGTCAA 2580

QY 653 ----- 653
Db 2581 ATTACAGACTTCGGGCTGGCTCGGCTGTGGACATTGACGACAGAGATPACCATGCAGAT 2640

QY 653 ----- 653
Db 2641 GGGGGCAAGGTGCCCATCAAGTGGATGGCGCTGGAGTCCATTCTCCGCGCGGCTTACC 2700

QY 653 ----- 653
Db 2701 CACCAGAGTATGTGGAGTTATGGTGTGACTGTGTGGAGCTGATGACTTTTGGGGCC 2760

QY 653 ----- 653
Db 2761 AAACCTTACGATGGGATCCAGCCCGGGAGATCCCTGACCTGCTGGAAAGGGGAGCGG 2820

QY 653 ----- 653
Db 2821 CTGCCCCAGCCCCCATCTGCACCATTGATGCTCTACATCATGTCGTCAAATGTTGGATG 2880

QY 653 ----- 653
Db 2881 ATTGACTCTGAATGTGCGCCAAGATTCCGGGAGTTGGTGTCTGAAATTCTCCCGCATGGCC 2940

QY 654 -----GlnAenGluAspLeuGlyProAlaSerProLeu 664
Db 2941 AGGGACCCCGACGCGCTTTGTGGTCAATCCAGATAGGACTTGGGCCCGACCCAGTCCCTTG 3000

QY 665 AspSerThrPheTyrArgSerLeuGluAspAspMetGlyAspLeuValAspAla 684
Db 3001 GACAGACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGACCTGGTGGATGCT 3060

QY 685 GluGluTyrLeuValProGlnGlnGlyPhePheCysProAspProAlaProGlyAlaGly 704
Db 3061 GAGGAGTATCTGGTACCACCGCAGCAGGGCTTCTTCTGCAGACCTGCCCGCGCGCTGG 3120

RESULT 12
US-09-441-411-5
; Sequence 5, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033-409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-441-411-5

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 10 Gaps: 1

US-09-493-480-7 (1-712) x US-09-441-411-5 (1-4473)

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Db 475 ATTGTGCGAGGACCCAGCTCTTTGAGGACAACATATGCTGCTGCGCGTGTAGACAAATGA 534
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Qy 141 GlnLeuArgSerLeuThrGluIleLeuLysGlyValLeuIleGlnArgAsnProGln 160
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RESULT 15

US-10-101-510-81
; Sequence 81, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR FILING DATE: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-81

Alignment Scores:
Pred. No.: 0 Length: 4473
Score: 3776.00 Matches: 712
Percent Similarity: 67.94% Conservative: 0
Best Local Similarity: 67.94% Mismatches: 0
Query Match: 95.50% Indels: 336
DB: 15 Gaps: 1

US-09-493-480-7 (1-712) x US-10-101-510-81 (1-4473)

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